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<110> English, Leigh H.
       Brussock, Susan M.
      Malvar, Thomas M.
       Bryson, James W.
       Kulesza, Caroline A.
       Walters, Frederick S.
       Slatin, Stephen L.
       Von Tersch, Michael A.
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Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
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	tcc tgg aag aaa ttt Ser Trp Lys Lys Phe 150		
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	tat gca caa gct gca Tyr Ala Gln Ala Ala 200		
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Thr Glu Asp Se	er Ser Thr	Glu Val I 55	Leu Asp	Asn Ser 60	Thr Val	Lys A	sp
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Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

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485 490 495

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Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr.Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605

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cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45	144
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	-	_	-	_	-	tct Ser 455		_			_		-			1392
-	_			-		gca Ala		-		_					-	1440
_			_	_	_	cgt Arg	-									1488
		-	_	_	_	ttt Phe					_	_	_	_		1536
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- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
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- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Leu Ser Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

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- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp $370 \hspace{1cm} 375 \hspace{1cm} 380$
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- Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430
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Tyr Ile Asn Lys 595	Thr Met A	sn Lys Asp 7	Asp Asp Leu	Thr Tyr 605	Gln Thr
Phe Asp Leu Ala 610		sn Ser Asn I 15	Met Gly Phe 620	Ser Gly	Asp Lys
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_						_		-	_					ttg Leu		6	524
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- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
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- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Pro Glu 210 215 220
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- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270
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- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 . 295 300
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- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
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410
415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly $435 \hspace{1.5cm} 440 \hspace{1.5cm} 445$

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr
565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645

<210> 7

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

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Leu Phe Leu Pro Thr Tyr Ala Gln Ala Asn Thr His Leu Leu Leu

		195					200				205				
													tca Ser		672
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	_												tta Leu 255	_	768
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_				-		-			-				tat Tyr	_	864
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		-								_			gga Gly		960
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													tac Tyr		1056
		_									-	-	act Thr	-	1104
	-				_	_							gga Gly	_	1152
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													ggt Gly 415		1248
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		-		-		caa Gln			_			_				1	.344
		-				tct Ser 455		-			-		-			1	.392
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		_		_	-	ttt Phe					-	_	_	_		1	.536
				-		aaa Lys	_		-					-		1	.584
		_				ttc Phe 535										1	.632
						gct Ala										1	.680
-	_			_		cgt Arg	_	_		_		-				1	728
		-				caa Gln					-			-		1	.776
					_	aat Asn		_	-	_						1	824
	_		_			aat Asn 615			_			_		-		1	872
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- <210> 8
- <211> 652
- <212> PRT
- <213> Artificial sequence
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- <223> Recombinant delta endotoxin
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- Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45
- Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
- Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80
- Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95
- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg

245 250 255

Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Ser	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln
Lys	Asn	Glu 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly
His	Val 450	Ser	Ala	Gln	Asp	Ser 455	Ile	Asp	Gln	Leu	Pro 460	Pro	Glu	Thr	Thr
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Cys	Phe	Leu	Met	Gln 485	Asp	Arg	Arg	Gly	Thr 490	Ile	Pro	Phe	Phe	Thr 495	Trp
Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser
Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys
Glu	Ser	Ser	Asn	Ser	Ile	Ala	Lys	Phe	Lys	Val	Thr	Leu	Asn	Ser	Ala

H: 532973(BF8T01!.DOC) 22

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Asn Leu Arg Leu Phe 580	Val Gln Asn Ser Asn 585	Asn Asp Phe Leu Val 590	Ile
Tyr Ile Asn Lys Thr 595	Met Asn Lys Asp Asp 600	Asp Leu Thr Tyr Gln 605	Thr
Phe Asp Leu Ala Thr 610	Thr Asn Ser Asn Met 615	Gly Phe Ser Gly Asp 620	Lys
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<221> CDS <222> (1)(1956) <400> 9 atg aat cca aac aat Met Asn Pro Asn Asn 1 5 aac agt gaa ttg caa Asn Ser Glu Leu Gln 20 cca aat tca aca cta Pro Asn Ser Thr Leu 35 act gaa gac agt tct	Arg Ser Glu His Asp . 10 act aac cat aat caa Thr Asn His Asn Gln 25 gaa gaa tta aat tat Glu Glu Leu Asn Tyr 40 acg gaa gtg cta gac	Thr Ile Lys Val Thr 15 tat cct tta gct gac Tyr Pro Leu Ala Asp 30 aaa gaa ttt tta aga Lys Glu Phe Leu Arg	Pro aat 96 Asn atg 144 Met gat 192
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H: 532973(BF8T01!.DOC) 23

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		aaa ata gag gag ta Lys Ile Glu Glu Ty 12	r Ala Lys Ser
_		ctt caa aat aat tt Leu Gln Asn Asn Ph 140	= =
		aaa aca cct tta ag Lys Thr Pro Leu Se 155	
		gaa ctt ttt tct ca Glu Leu Phe Ser Gl 170	
	Ser Met Pro Ser	ttt gca gtt tcc aa Phe Ala Val Ser Ly 185	
_		gct gca aat aca ca Ala Ala Asn Thr Hi 20	s Leu Leu Leu
		gaa gaa tgg gga ta Glu Glu Trp Gly Ty 220	
	-	caa tta aaa ctt ac Gln Leu Lys Leu Th 235	
-		aat gtt gga tta aa Asn Val Gly Leu As 250	
	Asp Ala Trp Val	aaa ttt aac cgt tt Lys Phe Asn Arg Ph 265	
		att gta ctt ttc cc Ile Val Leu Phe Pr 28	o Phe Tyr Asp
		aaa aca gaa cta ac Lys Thr Glu Leu Th 300	
		aat act ctt cag ga Asn Thr Leu Gln Gl 315	

H: 532973(BF8T01!.DOC)

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					agt Ser							1152
					gta Val 390							1200
					aat Asn							1248
					acg Thr							1296
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	_	-			gat Asp							1392
-	-			-	aaa Lys 470	_	_					1440
					gac Asp							1488
					gac Asp							1536
					gtg Val							1584
		_			gga Gly							1632

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			caa Gln													1728
			ctt Leu 580								_			_		1776
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<213 <213 <221 <220 <400 Met 1 Asn	1> (2) (2) (3) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4	652 PRT Artin Recor 10 Pro Glu Ser 35	Asn Leu 20	Asn 5 Gln Leu	Arg Thr	Ser Asn Glu	Glu His Leu 40	His Asn 25 Asn	10 Gln Tyr	Tyr Lys	Pro Glu	Leu Phe 45	Ala 30 Leu	15 Asp Arg	Asn Met	
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- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr Asn Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Ser Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp $370 \hspace{1cm} 375 \hspace{1cm} 380 \cdot$
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405
410
415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

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His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
180 185 190

ctg ttt cta cca aca tat gca caa gct gca aat aca cat tta ttg cta
Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu
195 200 205

cat ttt cgt aat tcc atg ccg tca ttt gca gtt tcc aaa ttc gaa gtg

576

			_		gtt Val			_	-						_	672
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					aaa Lys		_									912
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					gaa Glu											1008
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		-			aat Asn							-				1104
	_				agt Ser	_									-	1152
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tat	Ser cga	Thr	Glu	Pro gct	Val 390 aat Asn	Gln	Lys gac	Leu gta	Ser	Phe 395 gct	Asp tgg	Gly	aat	ggt	400 aag	1248

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- Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
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- Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95
- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr Thr Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
 245 250 255

Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe · 305	Thr	Asp	Pro	Ile	Phe 310	Ser	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln
Lys	Asn	Glu 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly
His	Val 450	Ser	Ala	Gln	Asp	Ser 455	Ile	Asp	Gln	Leu	Pro 460	Pro	Glu	Thr	Thr
Asp 465	Glu	Pro	Leu	Glu	Lys 470	Ala	Tyr	Ser	His	Gln 475	Leu	Asn	Tyr	Ala	Glu 480
Cys	Phe	Leu	Met	Gln 485	Asp	Arg	Arg	Gly	Thr 490	Ile	Pro	Phe	Phe	Thr 495	Trp
Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser
Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys
Glu 545	Ser	Ser	Asn	Ser	Ile 550	Ala	Lys	Phe	Lys	Val 555	Thr	Leu	Asn	Ser	Ala 560

1	Ala	Leu	Leu	Gln	Arg 565	Tyr	Arg	Val	Arg	Ile 570	Arg	Tyr	Ala	Ser	Thr 575	Thr	
Ž	Asn	Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
ŗ	Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
]	Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
	Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
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7		-					tct Ser	-	_		_				_	_	240
							gca Ala										288

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					ata Ile											384
					tta Leu											432
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	-	_		-	cga Arg			_					-	_	-	528
		_			atg Met	_			-	-				-		576
_					tat Tyr	-		_	-					_		624
		_	-		gtt Val				-						-	672
-	_	-	_		tat Tyr 230		_									720
	_		_	_	aat Asn				_						_	768
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					aaa Lys											912
	_	_			ttt Phe 310						_					960

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	tta Leu															1056
	aaa Lys	-										-	-		_	1104
	agt Ser 370															1152
	tct Ser		-		-		_		_		-				-	1200
	cga Arg			_			-	_		_		_			-	1248
_	tat Tyr			-	_		_	_		-			-	-		1296
	aat Asn	_		-					_			_				1344
	gta Val 450	_	_	_	_			_			_		-			1392
-	gaa Glu			_		_		_		_					_	1440
	ttc Phe															1488
	cat His															1536
	caa Gln															1584
	att Ile 530															1632
gaa	tct	agt	aat	tca	att	gct	aaa	ttt	aaa	gtt	aca	tta	aat	tca	gca	1680

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560	
gcc ttg tta caa cga tat cgt gta aga ata cgc tat gct tct acc act 'Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575	1728
aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	1776
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605	1824
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620	1872
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Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys

405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 .

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 620

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		_	-		-	ttt Phe 215			-						-	672
_	_	_	_			cat His	_									720
			-	_		tgg Trp			-						_	768
				-	_	tgg Trp	_				_		_	-	-	816
						gat Asp										864
						ggg Gly 295	_			_			-	-		912
						tta Leu					_	_				960
		_	_		-	aac Asn			-						-	1008
						ttt Phe		_	_							1056
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	_				_	aag Lys 375									_	1152
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41

Lys	Asn	Glu 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly	
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		-	-	-	-	ttt Phe						_	_			1536
						aaa Lys	_		_	_				_		1584
		_				ttc Phe 535										1632
-		-				gct Ala				-					-	1680
						cgt Arg										1728
						caa Gln					-			-		1776
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<212> PRT

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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

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Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 . 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile . 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575	•
Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	
Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605	
Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 620	
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	96
1 5 10 15 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn	96 144
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30 Cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met	
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20	144

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		gcg Ala					_					_	_	_	_	480
	-	agc Ser		-	_			-					-	-	-	528
		cgt Arg							-	-					-	576
		cta Leu 195														624
		gat Asp	_		_			-	-						_	672
_	-	gct Ala	-				_									720
		cat His														768
		act Thr														816
_		tta Leu 275		-					-						-	864
		tta Leu														912
	-	gat Asp									_	_	_			960
act	ttt	ttg	agt	ata	gaa	aac	tct	att	cga	aaa	cct	cat	tta	ttt	gat	1008

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					agt Ser											1152
			-		gta Val 390		_		_		_				-	1200
					aat Asn											1248
				-	acg Thr			-					-			1296
					aca Thr											1344
	-	_	_	_	gat Asp			-			_		-			1392
_	-			-	aaa Lys 470	-		_		-					-	1440
					gac Asp											1488
					gac Asp											1536
					gtg Val											1584
		_			gga Gly											1632
_		_			att Ile	_				-					-	1680

		550			555				560	
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tac att aat Tyr Ile Asn 595										1824 .
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Gln Val	Glu 115	Val	Leu	Ile	-	Lys 120	Lys	Ile	Glu	Tyr 125	Ala	Lys	Ser	

- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 . 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Thr Leu Asn Thr Leu Gln Lys Cys Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 380
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400
- Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645

<210> 19

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS <222> (1)..(1956)

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		Pro															40
	_	gaa Glu	_										_	_			96
		tca Ser 35														1	44
		gac Asp														1	92
		ggg Gly														2	40
_		cca Pro		_		_										2	88
		ata Ile				_		-			_	_		_	_	3	36
		gaa Glu 115														3	84
		ctt Leu														4	32
		gcg Ala														4	80
		agc Ser														5	28
		cgt Arg							-					-		5	76
		cta Leu 195														6	24
tta	aaa	gat	gct	caa	gtt	ttt	gga	gaa	gaa	tgg	gga	tat	tct	tca	gaa	6	72

Leu	Lys 210	Asp	Ala	Gln	Val	Phe 215	Gly	Glu	Glu	Trp	Gly 220	Tyr	Ser	Ser	Glu	
-	-	-	-		tat Tyr 230		_									720
					aat Asn											768
				-	gca Ala		-						-	-	_	816
-				-	tta Leu	_			_						_	864
					aaa Lys		-			_			_	-		912
					ttt Phe 310											960
					gaa Glu											1008
		_			gaa Glu			_	_							1056
		_			aat Asn							-	_		_	1104
					agt Ser											1152
					gta Val 390											1200
					aat Asn											1248
					acg Thr			-					-			1296
					aca Thr											1344

		435					440				445				
										ccg Pro 460		_			1392
_	_			_		_		_	_	ctt Leu				_	1440
_			_	_	-	_	_			cca Pro					1488
										gat Asp					1536
										tct Ser					1584
										tta Leu 540					1632
										aca Thr					1680
						_	_	_	_	tat Tyr	_				1728
										gat Asp			-		1776
_		_	_			_	_	_	 	tta Leu					1824
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						ttt Phe				ttg Leu	taa				1959

<210> 20 <211> 652

- <212> PRT
- <213> Artificial sequence
- <220>
- <223> Recombinant delta endotoxin
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- Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30
- Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45
- Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
- Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80
- Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95
- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu

Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile	Val	Leu	Phe	Pro	Phe	Tyr	Asp
		275					280					285			

260

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

265

270

Phe Thr Asp Pro Ile Phe Ala Val Asn Thr Leu Trp Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr

55

				565					570					575		
Ası	ı Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
Ту	: Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	e Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
As: 62:	n Glu 5	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
Ту	: Ile	Asp	Lys	Ile 645	Glu	Phe	Ile	Pro	Val 650	Gln	Leu					
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	20> 23> 1	Recoi	mbina	ant o	delta	a end	dotox	kin								
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	g aat : Asn															48
	agt Ser	-											-	_		96
	a aat o Asn															144
	gaa Glu 50															192
	gtt Val															240

H: 532973(BF8T01!.DOC)

85

90

288

336

95

gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu

aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca

Asn	Thr	Ile	Trp 100	Pro	Ser	Asp	Ala	Asp 105	Pro	Trp	Lys	Ala	Phe 110	Met	Ala	
					ata Ile											384
			_	_	tta Leu								-	_		432
_		_			tcc Ser 150		_					-	_	_	_	480
				_	cga Arg								_	_	-	528
		-			atg Met	_			_	_				_		576
_					tat Tyr	-		_	-					_		624
					gtt Val											672
					tat Tyr 230											720
					aat Asn				_						_	768
					gca Ala											816
_				-	tta Leu	_			_						_	864
					aaa Lys		_			-			_	_		912
					ttt Phe 310											960
					gaa Glu											1008

325	5	330	335
-	_	cgt ctt caa cct ggt Arg Leu Gln Pro Gly 350	Tyr Phe
		ggt aat tat gta gaa Gly Asn Tyr Val Glu 365	_
		act tcc cca ttt tat Thr Ser Pro Phe Tyr 380	
		agc ttt gat gga caa Ser Phe Asp Gly Gln 395	
	a Asn Thr Asp Val	gcg gct tgg ccg aat Ala Ala Trp Pro Asn 410	
		ttt agt caa tat gat Phe Ser Gln Tyr Asp 430	
-		gat tca aaa aga aac Asp Ser Lys Arg Asn 445	3 2
	_	caa tta ccg cca gaa Gln Leu Pro Pro Glu 460	
		cat cag ctt aat tac His Gln Leu Asn Tyr 475	
	n Asp Arg Arg Gly	aca att cca ttt ttt Thr Ile Pro Phe Phe 490	
		aca att gat gct gaa Thr Ile Asp Ala Glu 510	
		gcc ttg tct tca ggt Ala Leu Ser Ser Gly 525	
		gga aat tta cta ttc Gly Asn Leu Leu Phe 540	
		aaa gtt aca tta aat Lys Val Thr Leu Asn 555	

Ala Leu Leu	caa cg Gln Ar 56	g Tyr											1728
aac tta cga Asn Leu Arg													1776
tac att aat Tyr Ile Asn 595	Lys Th	_			_	_	_						1824
ttt gat ctc Phe Asp Leu . 610									_		-	_	1872
aat gaa ctt Asn Glu Leu 625													1920
tat ata gat Tyr Ile Asp		e Glu							taa				1959
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	ficial	seque	nce										
<213> Arti	ficial mbinant			dotoz	kin								
<213> Arti				dotoz	kin								
<213> Arti <220> <223> Reco	mbinant	delta	a end			Asp 10	Thr	Ile	Lys	Val	Thr 15	Pro	
<213> Arti <220> <223> Reco <400> 22 Met Asn Pro	mbinant Asn As 5	delta n Arg	ser Asn	Glu His	His Asn	10		Pro	Leu		15 Asp		
<213> Arti <220> <223> Reco <400> 22 Met Asn Pro 1	Asn As 5 Leu Gl 20	delta n Arg n Thr	ser Asn	Glu His	His Asn 25	10 Gln	Tyr	Pro	Leu	Ala 30	15 Asp	Asn	
<213> Arti <220> <223> Reco <400> 22 Met Asn Pro 1 Asn Ser Glu Pro Asn Ser	Asn As 5 Leu Gl 20 Thr Le	delta n Arg n Thr u Glu	Ser Asn Glu	Glu His Leu 40	His Asn 25 Asn	10 Gln Tyr	Tyr Lys	Pro Glu	Leu Phe 45	Ala 30 Leu	15 Asp Arg	Asn Met	
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- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg. 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400
- Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430 ·

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650

<210> 23

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

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cca aat tca Pro Asn Ser 35		-			s Glu		_	-	
act gaa gac Thr Glu Asp 50									
gca gtt ggg Ala Val Gly 65					n Ile			al	
gga gtt cca Gly Val Pro									
aac act ata Asn Thr Ile									
caa gtt gaa Gln Val Glu 115		_	_	_	.u Glu	_		-	
aaa gct ctt Lys Ala Leu 130									
gtt aat gcg Val Asn Ala 145					o Leu		Arg S		
aaa aga agc Lys Arg Ser	_	-				-	-	-	
cat ttt cgt His Phe Arg				_				-	
ctg ttt cta Leu Phe Leu 195					n Thr				
tta aaa gat Leu Lys Asp									

62

210	215	220
	-	

							ctt Leu			720
							tta Leu			768
							cgt Arg			816
							ttc Phe			864
							cta Leu 300			912
_	_		_				cag Gln	-		960
							cct Pro			1008
							caa Gln			1056
							tat Tyr			1104
							cca Pro 380			1152
							gat Asp			1200
-		_		_	_		tgg Trp			1248
							caa Gln			1296
	-	_				-	aaa Lys	-		 1344

	_	_	_	_	gat Asp			_					_			1392
_	-			-	aaa Lys 470	_		_		-					-	1440
					gac Asp											1488
		-	_	_	gac Asp						•	_	-	_		1536
				_	gtg Val		-		-	-				-		1584
		_			gga Gly											1632
_					att Ile 550	_				-					-	1680
					tat Tyr											1728
					gtg Val											1776
					atg Met			-	_	-						1824
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			_		gaa Glu				-			taa				1959

<210> 24 <211> 652 <212> PRT <213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 24

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270

Met	Thr	Leu 275	Thr			Asp		Ile	Val	Leu		Pro 285	Phe	Tyr	Asp	
т1.	7	T	m	Com	T	G1	77 - J	T	m\	G1	T	m1	7	7	~ 1	

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

Phe Thr Asp Pro Ile Phe Thr Pro Thr Thr Leu Gln Asp Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

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Tyr Ile As	_	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe Asp Le	u Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
Asn Glu Le	u Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
Tyr Ile As	p Lys	Ile 645	Glu	Phe	Ile	Pro	Val 650	Gln	Leu					
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atg aat co Met Asn Pr 1 aac agt ga	a ttg u Leu 20 a aca r Thr	Asn 5 caa Gln cta	act Thr	ser aac Asn	Glu cat His	His aat Asn 25 aat	Asp 10 caa Gln tat	Thr tat Tyr	Ile cct Pro	Lys tta Leu ttt	Val gct Ala 30 tta	Thr 15 gac Asp	Pro aat Asn	
atg aat co Met Asn Pr 1 aac agt ga Asn Ser Gl	a ttg u Leu 20 a aca r Thr	Asn 5 caa Gln cta Leu tct	act Thr gaa Glu	ser aac Asn gaa Glu	Glu cat His tta Leu 40	aat Asn 25 aat Asn	Asp 10 caa Gln tat Tyr	Thr tat Tyr aaa Lys	cct Pro gaa Glu	tta Leu ttt Phe 45 aca	yal gct Ala 30 tta Leu	Thr 15 gac Asp aga Arg	Pro aat Asn atg Met	96
atg aat co Met Asn Pr 1 aac agt ga Asn Ser Gl cca aat to Pro Asn Ser act gaa ga Thr Glu As	a ttg u Leu 20 a aca r Thr c agt p Ser	Asn 5 caa Gln cta Leu tct Ser gga	act Thr gaa Glu acg Thr	ser aac Asn gaa Glu gaa Glu 55 tct	Glu cat His tta Leu 40 gtg Val	His aat Asn 25 aat Asn cta Leu gta	Asp 10 caa Gln tat Tyr gac Asp	Thr tat Tyr aaa Lys aac Asn cag	cct Pro gaa Glu tct Ser 60	tta Leu ttt Phe 45 aca Thr	Val gct Ala 30 tta Leu gta Val	Thr 15 gac Asp aga Arg aaa Lys	Pro aat Asn atg Met gat Asp	96 144
atg aat co Met Asn Pr 1 aac agt ga Asn Ser Gl cca aat to Pro Asn Ser 35 act gaa ga Thr Glu As 50 gca gtt gg Ala Val Gl	a ttg u Leu 20 a aca r Thr c agt p Ser g aca y Thr a ttt	Asn 5 caa Gln cta Leu tct ser gga Gly gct	Arg act Thr gaa Glu acg Thr att Ile 70 ggg	Ser aac Asn gaa Glu gaa Glu 55 tct Ser gca	Glu cat His tta Leu 40 gtg Val gtt Val	His aat Asn 25 aat Asn cta Leu gta Val act	Asp 10 caa Gln tat Tyr gac Asp	Thr tat Tyr aaa Lys aac Asn cag Gln 75 ttt	Cct Pro gaa Glu tct Ser 60 att Ile	tta Leu ttt Phe 45 aca Thr tta Leu	yal gct Ala 30 tta Leu gta Val ggt Gly tca	Thr 15 gac Asp aga Arg aaa Lys gtt Val	Pro aat Asn atg Met gat Asp gta Val 80 ctt	96 144 192

			100					105					110			
caa ç Ğln V	_	-	-	-		-					-					384
aaa q Lys <i>I</i>	_		_			_	_									432
gtt a Val <i>I</i> 145							_					_	_	-	•	480
aaa a Lys <i>F</i>	_	_		-	_			-					-	_	_	528
cat t His E																576
ctg t Leu I						-		_	-					_		624
tta a Leu I		_	_		_			-	_						-	672
gat o Asp V 225	-	-	_				_									720
act o																768
ggt t Gly S																816
atg a Met 1				-		-			-						-	864
att o							_			_			-	_		912
ttt a Phe 1 305	_					-					_					960
act t Thr E		-	-		-				_						_	1008

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					acg Thr							1296
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	-	_	_	_	gat Asp		-					1392
					aaa Lys 470							1440
					gac Asp							1488
					gac Asp							1536
					gtg Val							1584
					gga Gly							1632
_		_			att Ile 550	_		-			-	1680

Ala Leu Leu	caa cga Gln Arg 565											1728
aac tta cga Asn Leu Arg												1776
tac att aat Tyr Ile Asn 595												1824
ttt gat ctc Phe Asp Leu 610		Thr A										1872
aat gaa ctt Asn Glu Leu 625			-			_			_			1920
tat ata gat Tyr Ile Asp	-	-			_		_	taa				1959
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115 120 125

Lys	Ala 130	Leu	Ala	Glu	Leu	Gln 135	Gly	Leu	Gln	Asn	Asn 140	Phe	Glu	Asp	Tyr
Val 145	Asn	Ala	Leu	Asn	Ser 150	Trp	Lys	Lys	Thr	Pro 155	Leu	Ser	Leu	Arg	Ser 160
Lys	Arg	Ser	Gln	Asp 165	Arg	Ile	Arg	Glu	Leu 170	Phe	Ser	Gln	Ala	Glu 175	Ser
His	Phe	Arg	Asn 180	Ser	Met	Pro	Ser	Phe 185	Ala	Val	Ser	Lys	Phe 190	Glu	Val
Leu	Phe	Leu 195	Pro	Thr	Tyr	Ala	Gln 200	Ala	Ala	Asn	Thr	His 205	Leu	Leu	Leu
Leu	Lys 210	Asp	Ala	Gln	Val	Phe 215	Gly	Glu	Glu	Trp	Gly 220	Tyr	Ser	Ser	Glu
Asp 225	Val	Ala	Glu	Phe	Tyr 230	His	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Tyr 240
Thr	Asp	His	Cys	Val 245	Asn	Trp	Tyr	Asn	Val 250	Gly	Leu	Asn	Gly	Leu 255	Arg
Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
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Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Ala	Leu	Asn	Thr	Leu 315	Asp	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
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H: 532973(BF8T01!.DOC)

71

420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

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<210> 27

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

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	_	-	_		act Thr							_	_		9(
					gaa Glu	_					-		_	_	144
					acg Thr										192
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					agt Ser										33)
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		_	_		gtt Val				-	_					67:

-	_	-	-		tat Tyr 230		_								720
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		_	_		gaa Glu				_					-	1008
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	_				agt Ser	-								 -	1152
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	_				aat Asn		_	-		-		_		 _	1248
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_			_	_	-	_	_	gga Gly								1488
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		_						gga Gly								1632
						_		ttt Phe		-					-	1680
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		-						tca Ser 585			-			_		1776
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<220>

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Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
245
250
255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285

Thr Arg Arg Phe Arg Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys $405 \hspace{1.5cm} 410 \hspace{1.5cm} 415$

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn	Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
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			20				1110	Asn 25	Gln		Pro					
			aca	cta	gaa	gaa	tta	25 aat	tat	Tyr		Leu ttt	Ala 30 tta	Asp	Asn	144
Pro	Asn gaa	Ser 35 gac	aca Thr	cta Leu tct	gaa Glu acg	gaa Glu gaa	tta Leu 40 gtg	25 aat Asn	tat Tyr gac	Tyr aaa Lys aac	Pro gaa	ttt Phe 45 aca	Ala 30 tta Leu gta	Asp aga Arg aaa	Asn atg Met	
Pro act Thr	Asn gaa Glu 50 gtt	Ser 35 gac Asp	aca Thr agt Ser	cta Leu tct Ser	gaa Glu acg Thr	gaa Glu gaa Glu 55	tta Leu 40 gtg Val	25 aat Asn cta Leu gta	tat Tyr gac Asp	Tyr aaa Lys aac Asn cag	Pro gaa Glu tct Ser	ttt Phe 45 aca Thr	Ala 30 tta Leu gta Val	Asp aga Arg aaa Lys	Asn atg Met gat Asp	144
Pro act Thr gca Ala 65	Asn gaa Glu 50 gtt Val	Ser 35 gac Asp ggg Gly	aca Thr agt Ser aca Thr	cta Leu tct Ser gga Gly	gaa Glu acg Thr att Ile 70	gaa Glu gaa Glu 55 tct Ser	tta Leu 40 gtg Val gtt Val	25 aat Asn cta Leu gta Val act	tat Tyr gac Asp ggg Gly	Tyr aaa Lys aac Asn cag Gln 75 ttt	gaa Glu tct Ser 60	ttt Phe 45 aca Thr tta Leu	Ala 30 tta Leu gta Val ggt Gly	Asp aga Arg aaa Lys gtt Val	Asn atg Met gat Asp gta Val 80 ctt	144 192

										gag Glu				384
										aat Asn 140				. 432
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										tct Ser				528
		_			_	_		-	_	tcc Ser		-		576
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										ttc Phe				864
						-			-	cta Leu 300	-	_		912
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					_			_		cct Pro			-	1008

					gaa Glu											1056
					aat Asn											1104
					agt Ser											1152
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					aat Asn						_	-			_	1248
-				_	acg Thr		-	-		_			_	_		1296
		_			aca Thr				_			-				1344
		-			gat Asp			-			_		_			1392
					aaa Lys 470					_					_	1440
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		_	_	-	gac Asp						-	_	_	_		1536
					gtg Val				_	-				-		1584
		-			gga Gly											1632
-		-			att Ile 550	-				_					_	1680
gcc	ttg	tta	caa	cga	tat	cgt	gta	aga	ata	cgc	tat	gct	tct	acc	act	1728

Ara bed bed o	Gln Arg 565	Tyr Arg	Val	-	Ile Ar	g Tyr	Ala	Ser	Thr 575	Thr	
aac tta cga c Asn Leu Arg I			Asn			-			-		1776
tac att aat a Tyr Ile Asn I 595											1824
ttt gat ctc g Phe Asp Leu A 610											1872
aat gaa ctt a Asn Glu Leu I 625	le Ile					l Ser					1920
tat ata gat a Tyr Ile Asp I	-	-		Pro V	-	_	taa				1959
<210> 30 <211> 652 <212> PRT <213> Artifi	cial se	quence									
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T T I	oinant d	lelta en	dotox	in							
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Lys	Ala 130	Leu	Ala	Glu	Leu	Gln 135	Gly	Leu	Gln	Asn	Asn 140	Phe	Glu	Asp	Tyr
Val 145	Asn	Ala	Leu	Asn	Ser 150	Trp	Lys	Lys	Thr	Pro 155	Leu	Ser	Leu	Arg	Ser 160
Lys	Arg	Ser	Gln	Asp 165	Arg	Ile	Arg	Glu	Leu 170	Phe	Ser	Gln	Ala	Glu 175	Ser
His	Phe	Arg	Asn 180	Ser	Met	Pro	Ser	Phe 185	Ala	Val	Ser	Lys	Phe 190	Glu	Val
Leu	Phe	Leu 195	Pro	Thr	Tyr	Ala	Gln 200	Ala	Ala	Asn	Thr	His 205	Leu	Leu	Leu
Leu	Lys 210	Asp	Ala	Gln	Val	Phe 215	Gly	Glu	Glu	Trp	Gly 220	Tyr	Ser	Ser	Glu
Asp 225	Val	Ala	Glu	Phe	Tyr 230	Arg	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Tyr 240
Thr	Asp	His	Cys	Val 245	Asn	Trp	Tyr	Asn	Val 250	Gly	Leu	Asn	Gly	Leu 255	Arg
Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Leu	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln

Lys Asn Glu Thr Ser Thr,Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650

<210> 31

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

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	agt Ser	-	-										-	-		96
	aat Asn															144
	gaa Glu 50															192
	gtt Val							-		_				_	-	240
	gtt Val			-		_										288
	act Thr						-	_			_	_		_	-	336
	gtt Val	_	-	_			_				_		-		_	384
	gct Ala 130					_							-	-		432
-	aat Asn			Asn			-					_	_	_	_	480
	aga Arg															528
	ttt Phe	_			-	_			_	-				_		576
	ttt Phe					-		-	-					_		624
	aaa Lys 210	_	-		_			_	-						_	672

Ā:		-	-	-			cat His	_									720
		-		_	•		tgg Trp			-						_	768
-	-				-	-	tgg Trp	_				-		_	_	_	816
							gat Asp										864
	le A						ggg Gly 295	-			_			_	_		912
Pł		-	-				atc Ile			-		_					960
							aac Asn										1008
			-			-	ttt Phe		_	_							1056
			_				tat Tyr						_	-		-	1104
	co S						aag Lys 375									-	1152
Ly							caa Gln										1200
							aca Thr										1248
_					-	-	aaa Lys	-	-		_			_	_		1296
							caa Gln										1344
Ca	at g	gta	agt	gca	cag	gat	tct	att	gac	caa	tta	ccg.	сса	gaa	aca	aca	1392

His	Val 450	Ser	Ala	Gln	Asp	Ser 455	Ile	Asp	Gln	Leu	Pro 460	Pro	Glu	Thr	Thr	
gat Asp 465				-		_		_		_					-	1440
tgt Cys																1488
aca Thr		-	-	-	-						_	-	_	_		1536
act Thr				-			-		-	_				_		1584
att Ile		_														1632
gaa Glu 545																1680
gcc Ala	_			_		-	-	_		-		-				1728
aac Asn		_									_			-		1776
tac Tyr																1824
ttt Phe																1872
aat Asn 625																1920
tat Tyr												taa				1959

<210> 32 <211> 652

<212> PRT <213> Artificial sequence

<223> Recombinant delta endotoxin

<400> 32

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp

275	280	285

Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Ile	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln
Lys	Asn	Glu 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly
His	Val 450	Ser	Ala	Gln	Asp	Ser 455	Ile	Asp	Gln	Leu	Pro 460	Pro	Glu	Thr	Thr
Asp 465	Glu	Pro	Leu	Glu	Lys 470	Ala	Tyr	Ser	His	Gln 475	Leu	Asn	Tyr	Ala	Glu 480
Cys	Phe	Leu	Met	Gln 485	Asp	Arg	Arg	Gly	Thr 490	Ile	Pro	Phe	Phe	Thr 495	Trp
Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser
Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys
Glu 545	Ser	Ser	Asn	Ser	Ile 550	Ala	Lys	Phe	Lys	Val 555	Thr	Leu	Asn	Ser	Ala 560
			Gln	565					570		_			575	
Asn	Leu	Arg	Leu	Phe	Val	Gln	Asn	Ser	Asn	Asn	Asp	Phe	Leu	Val	Ile

580 585 590 Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 600 Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 615 Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 635 Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 <210> 33 <211> 1959 <212> DNA <213> Artificial sequence <220> <223> Recombinant delta endotoxin <220> <221> CDS <222> (1)..(1956)<400> 33 atg aat cca aac aat cga agt gaa cat gat acg ata aag gtt aca cct Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro

48 10 aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat 96 Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg 144 Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 act gaa gac agt tot acg gaa gtg cta gac aac tot aca gta aaa gat 192 Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta 240 Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt 288 Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca 336

H: 532973(BF8T01!.DOC)

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
100 105 110

						gat Asp										384
						cag Gln 135										432
						tgg Trp										480
						ata Ile										528
						ccg Pro										576
						gca Ala		-	_					_		624
						ttt Phe 215										672
						cat His	_									720
						tgg Trp										768
						tgg Trp										816
_				-		gat Asp			-						_	864
						ggg Gly 295										912
						atc Ile										960
					-	aac Asn			_						-	1008
tat	tta	cag	ggg	att	gaa	ttt	cat	acg	cgt	ctt	caa	cct	ggt	tac	ttt	1056

H: 532973(BF8T01!.DOC)

Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe		
					aat Asn											1	104
					agt Ser											1	.152
					gta Val 390											1	.200
					aat Asn											1	.248
					acg Thr											1	.296
					aca Thr				_			_				1	.344
					gat Asp								_			1	.392
					aaa Lys 470					_					-	1	440
					gac Asp											1	.488
					gac Asp											1	.536
					gtg Val											1	.584
					gga Gly											1	632
-		_			att Ile 550	_				-					_	1	680
	_			_	tat Tyr	-	_	_		_		-				1	728

	565	570	575
-	Phe Val Gln Asn Se	ca aac aat gat ttt ct er Asn Asn Asp Phe Le 85	u Val Ile
	_	at gat gat tta aca ta sp Asp Asp Leu Thr Ty 605	
		at atg ggg ttc tcg gg sn Met Gly Phe Ser Gl 620	
_		ct ttc gtt tct aat ga er Phe Val Ser Asn Gl 635	
	ata gaa ttt atc co Ile Glu Phe Ile Pr 645		1959
<210> 34 <211> 652 <212> PRT <213> Artifici	al sequence		
<220			
<220> <223> Recombin	ant delta endotoxir	n	
	ant delta endotoxir	n	
<223> Recombin <400> 34		s Asp Thr Ile Lys Va 10	l Thr Pro 15
<223> Recombin <400> 34 Met Asn Pro Asn 1	Asn Arg Ser Glu Hi 5	s Asp Thr Ile Lys Va 10 n Gln Tyr Pro Leu Al	15 a Asp Asn
<223> Recombin <400> 34 Met Asn Pro Asn 1 Asn Ser Glu Leu 20	Asn Arg Ser Glu Hi 5 Gln Thr Asn His As 25	s Asp Thr Ile Lys Va 10 n Gln Tyr Pro Leu Al	15 a Asp Asn
<223> Recombin <400> 34 Met Asn Pro Asn 1 Asn Ser Glu Leu 20 Pro Asn Ser Thr 35	Asn Arg Ser Glu Hi 5 Gln Thr Asn His As 25 Leu Glu Glu Leu As 40	sn Gln Tyr Pro Leu Al 30	15 a Asp Asn u Arg Met
<223> Recombin <400> 34 Met Asn Pro Asn 1 Asn Ser Glu Leu 20 Pro Asn Ser Thr 35 Thr Glu Asp Ser 50	Asn Arg Ser Glu His 5 Gln Thr Asn His As 25 Leu Glu Glu Leu As 40 Ser Thr Glu Val Le	as Asp Thr Ile Lys Va 10 sn Gln Tyr Pro Leu Al 5 30 sn Tyr Lys Glu Phe Le 45	15 a Asp Asn u Arg Met l Lys Asp
<223> Recombine <400> 34 Met Asn Pro Asn 1 Asn Ser Glu Leu 20 Pro Asn Ser Thr 35 Thr Glu Asp Ser 50 Ala Val Gly Thr 65	Asn Arg Ser Glu His 5 Gln Thr Asn His As 25 Leu Glu Glu Leu As 40 Ser Thr Glu Val Le 55 Gly Ile Ser Val Var 70	as Asp Thr Ile Lys Va 10 sn Gln Tyr Pro Leu Al 30 sn Tyr Lys Glu Phe Le 45 eu Asp Asn Ser Thr Va 60 al Gly Gln Ile Leu Gl	15 a Asp Asn u Arg Met l Lys Asp y Val Val 80
<223> Recombine <400> 34 Met Asn Pro Asn 1 Asn Ser Glu Leu 20 Pro Asn Ser Thr 35 Thr Glu Asp Ser 50 Ala Val Gly Thr 65 Gly Val Pro Phe	Asn Arg Ser Glu His 5 Gln Thr Asn His As 25 Leu Glu Glu Leu As 40 Ser Thr Glu Val Le 55 Gly Ile Ser Val Va 70 Ala Gly Ala Leu Th 85	as Asp Thr Ile Lys Variation Sin Gln Tyr Pro Leu Al 30 Sin Tyr Lys Glu Phe Le 45 Sin Asp Asn Ser Thr Va 60 Sil Gly Gln Ile Leu Gl 75 Ser Phe Tyr Gln Se 90 Sip Pro Trp Lys Ala Ph	a Asp Asn u Arg Met l Lys Asp y Val Val 80 r Phe Leu 95

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala	Glu Leu Gln Gly	Leu Gln Asn Asn Phe	Glu Asp Tyr
130	135	140	

- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Ile Leu His Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400
- Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415
- Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650

<210> 35

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 35

						agt Ser										48
	-	-	_			aac Asn							_	_		96
					-	gaa Glu					-			_	_	144
	-	_	_		_	gaa Glu 55			-				_		_	192
-	-					tct Ser	-	-		_				-	_	240
	-			-		gca Ala										288
					_	gat Asp	_	-			_	_		_	_	336
						gat Asp										384
	_		_	_		cag Gln 135							-	_		432
						tgg Trp							-			480
						ata Ile										528
						ccg Pro										576
						gca Ala										624
		-	-		-	ttt Phe 215		_	_						-	672
gat	gtt	gct	gaa	ttt	tat	cat	aga	caa	tta	aaa	ctt	aca	caa	caa	tac	720

Asp 225	Val	Ala	Glu	Phe	Tyr 230	His	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Tyr 240	
					aat Asn											768
				-	gca Ala		-				-		_	_	_	816
					tta Leu											864
					aaa Lys											912
					ttt Phe 310						_					960
		_	_		gaa Glu				_						_	1008
					gaa Glu											1056
					aat Asn							_	-		_	1104
					agt Ser											1152
			_		gta Val 390		-		_		-				-	1200
					aat Asn											1248
					acg Thr											1296
					aca Thr											1344
					gat Asp											1392

450 455 460

_	_			_		gca Ala		_		_					-	1440
						cgt Arg										1488
		-	_	_	_	ttt Phe					_	-	_	-		1536
				-		aaa Lys	_		-	-				_		1584
		_				ttc Phe 535										1632
_		_				gct Ala				-					-	1680
	_			_		cgt Arg						_				1728
		_				caa Gln					_			_		1776
						aat Asn										1824
	_		_			aat Asn 615			_	525		_		_		1872
	-					gca Ala	_			-			-			1920
		-	_		-	ttt Phe			-		_	taa				1959

<210> 36

<211> 652

<212> PRT <213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 36

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285

Ile	Arg 290	Leu	_		Lys	 Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
				_										

- Phe Thr Asp Pro Ile Phe Ser Leu Val Asn Leu Met Val Tyr Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp $370 \hspace{1cm} 375 \hspace{1cm} 380$
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400
- Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415
- Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430
- Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445
- His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460
- Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480
- Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
 485 490 495
- Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510
- Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525
- Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540
- Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560
- Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575
- Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Ġly	Asp	Lys	
Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
Tyr	Ile	Asp	Lys	Ile 645	Glu	Phe	Ile	Pro	Val 650	Gln	Leu					
<210 <211 <212 <213 <220 <223	.> : ?> ! }> <i>!</i>			al se	-		doto:	kin								
<220 <221 <222	.> (CDS	. (195	56)												
	aat			aat Asn 5												48
				caa Gln												96
				cta Leu							-			_	_	144
	_	_	_	tct Ser	_	_			-				_		-	192
gca Ala 65				gga Gly												240
gga Gly				gct Ala 85												288
aac Asn					-	-	_	-			_	_		_	-	336
caa	gtt	gaa	gta	ctg	ata	gat	aag	aaa	ata	gag	gag	tat	gct	aaa	agt	384

Gln	Val	Glu 115	Val	Leu	Ile	Asp	Lys 120	Lys	Ile	Glu	Glu	Tyr 125	Ala	Lys	Ser	
	_		-	-		cag Gln 135	_						-			432
_						tgg Trp	-					_	_	-	-	480
	-	_		-	_	ata Ile		-					_	_	_	528
		_			_	ccg Pro			-	_				-		576
_						gca Ala		-	-					-		624
		_	-		-	ttt Phe 215		-	-						_	672
-	_	_	-			cat His	_									720
	_		_	_		tgg Trp			-						_	768
				-	_	tgg Trp					-		_	_	_	816
						gat Asp										864
						ggg Gly 295										912
						tct Ser										960
		-			-	aac Asn			_						-	1008
		-			_	ttt Phe		_	_							1056

340	345	350

		-			aat Asn							-	_		_	1104
					agt Ser											1152
			_		gta Val 390		_								_	1200
	_			_	aat Asn		_	_		_		_			_	1248
-				_	acg Thr		_	-		-			-	_		1296
		_		_	aca Thr				-			_				1344
	-	-	_	_	gat Asp			-			_		-			1392
_	_			_	aaa Lys 470					_					_	1440
-			_	_	gac Asp	-	_									1488
		-	-	_	gac Asp						_	-	-	_		1536
					gtg Val											1584
					gga Gly											1632
					att Ile 550											1680
-	_				tat Tyr			_		_		_				1728

H: 532973(BF8T01!.DOC) 102

aac tta cga ctt ttt gtg caa aat tca aac aat gat ttt ctt gtc atc Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590	1776												
tac att aat aaa act atg aat aaa gat gat gat tta aca tat caa aca Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605	1824												
ttt gat ctc gca act act aat tct aat atg ggg ttc tcg ggt gat aag Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620	1872												
aat gaa ctt ata ata gga gca gaa tct ttc gtt tct aat gaa aaa atc Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640	1920												
tat ata gat aag ata gaa ttt atc cca gta caa ttg taa Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650	1959												
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130 135 140

Val 145	Asn	Ala	Leu	Asn	Ser 150	Trp	Lys	Lys	Thr	Pro 155	Leu	Ser	Leu	Arg	Ser 160
Lys	Arg	Ser	Gln	Asp 165	Arg	Ile	Arg	Glu	Leu 170	Phe	Ser	Gln	Ala	Glu 175	Ser
His	Phe	Arg	Asn 180	Ser	Met	Pro	Ser	Phe 185	Ala	Val	Ser	Lys	Phe 190	Glu	Val
Leu	Phe	Leu 195	Pro	Thr	Tyr	Ala	Gln 200	Ala	Ala	Asn	Thr	His 205	Leu	Leu	Leu
Leu	Lys 210	Asp	Ala	Gln	Val	Phe 215	Gly	Glu	Glu	Trp	Gly 220	Tyr	Ser	Ser	Glu
Asp 225	Val	Ala	Glu	Phe	Tyr 230	His	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Ту: 240
Thr	Asp	His	Cys	Val 245	Asn	Trp	Tyr	Asn	Val 250	Gly	Leu	Asn	Gly	Leu 255	Arg
Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Il€
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Ser	Leu	Arg	Thr	Pro 315	Leu	Ala	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arç
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln
Lvs	Asn	Glu	Thr	Ser	Thr	Gln	Thr	Tvr	Asp	Ser	Lvs	Ara	Asp	Asn	Gla

435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650

<210> 39

<211> 1959

<212> DNA

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<220>

<221> CDS

<222> (1)..(1956)

<400> 39

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48

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					_	gaa Glu					_			_	_		144
	-	_	-		-	gaa Glu 55									-		192
-	_					tct Ser	-			_				_	_		240
	_			_		gca Ala											288
						gat Asp					_	-		-	_		336
						gat Asp											384
						cag Gln 135											432
-						tgg Trp	_					_	_	-	_		480
				_		ata Ile							_	_	_		528
		_			_	ccg Pro			-	-				_			576
-						gca Ala		-	-					_			624
		_	_		_	ttt Phe 215		_	_						_		672
-	-	-	-			cat His										`	720

						tgg Trp										768
				_	_	tgg Trp	_				_		_		-	816
_						gat Asp			-							864
	-			-		ggg Gly 295	-			_			_			912
	_	_				tca Ser					_	-				960
		_	-		_	aac Asn			-						_	1008
						ttt Phe										1056
						tat Tyr										1104
	_				-	aag Lys 375									-	1152
			-		_	caa Gln	-		_		-				-	1200
						aca Thr										1248
						aaa Lys										1296
		_		_		caa Gln			_			_				1344
	-	-	_	_	_	tct Ser 455		-								1392
gat	gaa	сса	ctt	gaa	aaa	gca	tat	agt	cat	cag	ctt	aat	tac	gcg	gaa	1440

Asp 6	Glu	Pro	Leu	Glu	Lys 470	Ala	Tyr	Ser	His	Gln 475	Leu	Asn	Tyr	Ala	Glu 480		
tgt t Cys F			_	-	-	_	-										1488
aca c Thr H		_	_	-	-						_	_	_	_		•	1536
act c				_			-		-	_				_			1584
att a Ile I 5		_															1632
gaa t Glu S 545		_				_				_					_		1680
gcc t Ala I																	1728
aac t Asn I		-									_			-			1776
tac a Tyr I								-	_	_							1824
ttt g Phe A	_		-						_			_		_	_		1872
aat g Asn G 625																	1920
tat a Tyr I												taa					1959

<210> 40

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 40

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro 1 5 10 15

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala
100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg
245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Asn 275 280 285

Ile Leu Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr \cdot Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Asn Glu Leu Ile 625	e Ile Gly Ala G 630	lu Ser Phe Val 635	Ser Asn Glu Lys	s Ile 640
Tyr Ile Asp Lys	s Ile Glu Phe I 645	le Pro Val Gln 650	Leu	
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			cct tta gct gad Pro Leu Ala Asp 30	
		eu Asn Tyr Lys	gaa ttt tta aga Glu Phe Leu Arg 45	
			tct aca gta aaa Ser Thr Val Lys 60	
	- -		att tta ggt gtt Ile Leu Gly Val	=
			tat caa tca ttt Tyr Gln Ser Phe 95	
	Pro Ser Asp A		aag gct ttt atg Lys Ala Phe Met 110	
	. Leu Ile Ásp Ly		gag tat gct aaa Glu Tyr Ala Lys 125	

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

	_		-		tta Leu	_							-	-		432
_					tcc Ser 150		_					_	_	_	-	480
	-	_		_	cga Arg			-					_	_	_	528
					atg Met											576
-					tat Tyr				-					_		624
		-	_		gtt Val			_	-						_	672
-	-	_	_		tat Tyr 230		_									720
	_		-	_	aat Asn				_						_	768
					gca Ala						_		-	_	_	816
_					tta Leu	_			-						_	864
					aaa Lys											912
	_	-			ttt Phe 310						_					960
			_		gaa Glu				_						_	1008
		_			gaa Glu			_	_							1056
ggg	aaa	gat	tct	ttc	aat	tat	tgg	tct	ggt	aat	tat	gta	gaa	act	aga	1104

Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg	
	_				_	_	aca Thr								_	1152
					-		aag Lys		_		_				-	1200
	-			-			gac Asp	-		-		_			-	1248
							gtt Val									1296
		-		-			aca Thr 440		_			_				1344
	-	_	_	_	-		att Ile	-			_		-			1392
							tat Tyr							_	_	1440
-			_	_	-	_	cgt Arg									1488
							ttt Phe									1536
							gca Ala 520									1584
							aca Thr									1632
							aaa Lys									1680
-				-		_	gta Val	-		_		_				1728
							aat Asn									1776

		aat Asn 595														1824
	-	ctc Leu	-						_	,,,		_		_	-	1872
	_	ctt Leu				-	_			_			_			1920
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650

590

585

<210> 42

<211> 652

<212> PRT

<213> Artificial sequence

580

<220>

<223> Recombinant delta endotoxin

645

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu

<400> 42

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser

145					150					155					160
Lys	Arg	Ser	Gln	Asp 165	Arg	Ile	Arg	Glu	Leu 170	Phe	Ser	Gln	Ala	Glu 175	Ser
His	Phe	Arg	Asn 180	Ser	Met	Pro	Ser	Phe 185	Ala	Val	Ser	Lys	Phe 190	Glu	Val
Leu	Phe	Leu 195	Pro	Thr	Tyr	Ala	Gln 200	Ala	Ala	Asn	Thŗ	His 205	Leu	Leu	Leu
Leu	Lys 210	Asp	Ala	Gln	Val	Phe 215	Gly	Glu	Glu	Trp	Gly 220	Tyr	Ser	Ser	Glu
Asp 225	Val	Ala	Glu	Phe	Tyr 230	His	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Tyr 240
Thr	Asp	His	Суѕ	Val 245	Asn	Trp	Tyr	Asn	Val 250	Gly	Leu	Asn	Gly	Leu 255	Arg
Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Val 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Ser	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thṛ	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln
Lys	Asn	Glu 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr

	450					455					460					
Asp 465	Glu	Pro	Leu	Glu	Lys 470	Ala	Tyr	Ser	His	Gln 475	Leu	Asn	Tyr	Ala	Glu 480	
Cys	Phe	Leu	Met	Gln 485	Asp	Arg	Arg	Gly	Thr 490	Ile	Pro	Phe	Phe	Thr 495	Trp	
Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile	
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser	
Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys	
Glu 545	Ser	Ser	Asn	Ser	Ile 550	Ala	Lys	Phe	Lys	Val 555	Thr	Leu	Asn	Ser	Ala 560	
Ala	Leu	Leu	Gln	Arg 565	Tyr	Arg	Val	Arg	Ile 570	Arg	Tyr	Ala	Ser	Thr 575	Thr	
Asn	Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
Tyr	Ile	Asp	Lys	Ile 645	Glu	Phe	Ile	Pro	Val 650	Gln	Leu					
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					act Thr											96

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act of																192
gca (Ala ' 65	-						-	_		_				_	-	240
gga (Gly '																288
aac a Asn '																336
caa (Gln '																384
aaa d Lys i																432
gtt a Val A 145							_					_	_	_	-	480
aaa a Lys <i>l</i>	_	-			_			-					_	_	_	528
cat t		_			_	_			_	_				_		576
ctg t Leu l																624
tta a Leu l																672
gat q Asp V 225	_	_	_				_									720
act o	_		-	-					-						_	768

H: 532973(BF8T01!.DOC)

ggt t Gly S											_		_	_	-	816
atg a Met T				_		_			_						_	864
att c Ile A 2							_			_			_	_		912
ttt a Phe T 305		_									_	, ,				960
act t Thr F		-	_		-				-						_	1008
tat t Tyr L																1056
ggg a Gly L		_										_	~		_	1104
cct a Pro S 3	-				-	_									-	1152
aaa t Lys S 385			-		-		_		-		-				-	1200
tat c Tyr A	_			_			_	-		-		_			_	1248
gta t Val T																1296
aaa a Lys A		_		_					-			_				1344
cat g His V 4	-	-	-	-	-			_			_		_			1392
gat g Asp G 465																1440

tgt tt														1488
aca ca Thr Hi														1536
act ca Thr Gl			_			-		_				 _		1584
att at Ile Ile 53	e Glu						_							1632
gaa to Glu Se 545	_				_				_				-	1680
gcc tte Ala Le									-		_			1728
aac tta Asn Le	-									_		_		1776
tac at Tyr Il				-			-	-	-					1824
ttt ga Phe As _l 61	p Leu													1872
aat gaa Asn Gli 625														1920
tat ata Tyr Ile											taa			1959
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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro 1 $$ 5 $$ 10 $$ 15

- Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30
- Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45
- Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
- Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80
- Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95
- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640	
Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650	
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aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30	96
cca aat tca aca cta gaa gaa tta aat tat aaa gaa ttt tta aga atg Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45	144
act gaa gac agt tct acg gaa gtg cta gac aac tct aca gta aaa gat Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60	192
gca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80	240
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95	288
aac act ata tgg cca agt gat gct gac cca tgg aag gct ttt atg gca Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110	336
caa gtt gaa gta ctg ata gat aag aaa ata gag gag tat gct aaa agt Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser · 115 120 125	384
aaa gct ctt gca gag tta cag ggt ctt caa aat aat ttc gaa gat tat Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140	432

-					tcc Ser 150		_					_	_	_		480
					cga Arg								_	_	-	528
		-			atg Met	-			_	_				_		576
-					tat Tyr	_		-	_					_		624
		-	_		gtt Val			_	-						_	672
_	-	_	-		tat Tyr 230		_									720
					aat Asn											768
				-	gca Ala		-				-		_	-	_	816
					tta Leu											864
					aaa Lys		_			-			_	-		912
					ttt Phe 310											960
			_		gaa Glu				_						-	1008
					gaa Glu											1056
					aat Asn							-	_		_	1104

						aág Lys 375										1	1152
			-		-	caa Gln	-		_		-				-	1	1200
						aca Thr										1	1248
_						aaa Lys	_	_		_			_	_		1	1296
						caa Gln										1	L344
	-	_	_	_	-	tct Ser 455		-			_		_			1	1392
_	_			_		gca Ala		_		_					_	1	1440
-			_	_	-	cgt Arg	-									1	1488
		-	-	-	-	ttt Phe					_	_	_	_		1	1536
						aaa Lys	_		_	_				_		1	L584
		_				ttc Phe 535										1	632
_		_				gct Ala				_					_	1	1680
						cgt Arg				_		_				1	.728
		Arg				caa Gln					_			_		1	.776
tac	att	aat	aaa	act	atg	aat	aaa	gat	gat	gat	tta	aca	tat	caa	aca	1	824

Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
						aat Asn 615										1872
	Glu					gca Ala										1920
						ttt Phe						taa				1959
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Met 1	Asn	Pro	Asn	Asn 5	Arg	Ser	Glu	His	Asp 10	Thr	Ile	Lys	Val	Thr 15	Pro	
Asn	Ser	Glu	Leu 20	Gln	Thr	Asn	His	Asn 25	Gln	Tyr	Pro	Leu	Ala 30	Asp	Asn	
Pro	Asn	Ser 35	Thr	Leu	Glu	Glu	Leu 40	Asn	Tyr	Lys	Glu	Phe 45	Leu	Arg	Met	
Thr	Glu 50	Asp	Ser	Ser	Thr	Glu 55	Val	Leu	Asp	Asn	Ser 60	Thr	Val	Lys	Asp	
Ala 65	Val	Gly	Thr	Gly	Ile 70	Ser	Val	Val	Gly	Gln 75	Ile	Leu	Gly	Val	Val 80	
Gly	Val	Pro	Phe	Ala 85	Gly	Ala	Leu	Thr	Ser 90	Phe	Tyr	Gln	Ser	Phe 95	Leu	
Asn	Thr	Ile	Trp 100	Pro	Ser	Asp	Ala	Asp 105	Pro	Trp	Lys	Ala	Phe 110	Met	Ala	
Gln	Val	Glu 115	Val	Leu	Ile	Asp	Lys 120	Lys	Ile	Glu	Glu	Tyr 125	Ala	Lys	Ser	
Lys	Ala 130	Leu	Ala	Glu	Leu	Gln 135	Gly	Leu	Gln	Asn	Asn 140	Phe	Glu	Asp	Tyr	
Val 145	Asn	Ala	Leu	Asn	Ser 150	Trp	Lys	Lys	Thr	Pro 155	Leu	Ser	Leu	Arg	Asn 160	
Pro	His	Ser	Gln	Gly	Arg	Ile	Arg	Glu	Leu	Phe	Ser	Gln	Ala	Glu	Ser	

175	5
	175

His	Phe	Arg	Asn 180	Ser	Met	Pro	Ser	Phe 185	Ala	Val	Ser	Lys	Phe 190	Glu	Va]
Leu	Phe	Leu 195	Pro	Thr	Tyr	Ala	Gln 200	Ala	Ala	Asn	Thr	His 205	Leu	Leu	Leu
Leu	Lys 210	Asp	Ala	Gln	Val	Phe 215	Gly	Glu	Glu	Trp	Gly 220	Tyr	Ser	Ser	Glu
Asp 225	Val	Ala	Glu	Phe	Tyr 230	His	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Ty1 240
Thr	Asp	His	Cys	Val 245	Asn	Trp	Tyr	Asn	Val 250	Gly	Leu	Asn	Gly	Leu 255	Arg
Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Ser	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Ph∈
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Туr	Val 365	Glu	Thr	Arc
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Glr
Lys	Asn	G1u 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly
His	Val 450	Ser	Ala	Gln	Asp	Ser 455	Ile	Asp	Gln	Leu	Pro 460	Pro	Glu	Thr	Thr
Asp	Glu	Pro	Leu	Glu	Lys	Ala	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Ala	Glu

465	470	475	480
Cys Phe Leu Met Gln 485	_	hr Ile Pro Phe Phe T 90 4	Thr Trp 195
Thr His Arg Ser Val	Asp Phe Phe Asn Tl	hr Ile Asp Ala Glu L 510	Lys Ile
Thr Gln Leu Pro Val	Val Lys Ala Tyr A 520	la Leu Ser Ser Gly A 525	Ala Ser
Ile Ile Glu Gly Pro 530	Gly Phe Thr Gly G 535	ly Asn Leu Leu Phe L 540	Leu Lys
Glu Ser Ser Asn Ser 545	Ile Ala Lys Phe Ly 550	ys Val Thr Leu Asn S 555	Ser Ala 560
Ala Leu Leu Gln Arg 565		le Arg Tyr Ala Ser T 70 5	Thr Thr 575
Asn Leu Arg Leu Phe 580	Val Gln Asn Ser A 585	sn Asn Asp Phe Leu V 590	/al Ile
Tyr Ile Asn Lys Thr 595	Met Asn Lys Asp A: 600	sp Asp Leu Thr Tyr G 605	Gln Thr
Phe Asp Leu Ala Thr 610	Thr Asn Ser Asn Me 615	et Gly Phe Ser Gly A 620	Asp Lys
Asn Glu Leu Ile Ile 625	Gly Ala Glu Ser Pl 630	he Val Ser Asn Glu L 635	Lys Ile 640
Tyr Ile Asp Lys Ile 645		al Gln Leu 50	
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				acg Thr						192
				att Ile 70						240
				ggg Gly						288
				agt Ser						336
				ata Ile						384
				tta Leu						432
				tcc Ser 150						480
				cga Arg						528
				atg Met						576
				tat Tyr						624
				gtt Val						672
 _	_	_		tat Tyr 230	_					720
_		_	_	aat Asn		-			_	768

						tgg Trp										816
_				_		gat Asp			-						-	864
_						ggg Gly 295								-		912
	_	_				tca Ser					_					960
						aac Asn										1008
		_			_	ttt Phe		_	_							1056
		_				tat Tyr						-	_		-	1104
						aag Lys 375										1152
			_		-	caa Gln	-		-		_				_	1200
						aca Thr										1248
						aaa Lys										1296
						caa Gln										1344
	_	_	_	_	-	tct Ser 455					-		_			1392
-	-			-		gca Ala		_		_					-	1440
tgt	ttc	tta	atg	cag	gac	cgt	cgt	gga	aca	att	сса	ttt	ttt	act	tgg	1488

Cys Phe Leu Met	Gln Asp Arg 485	Arg Gly Thr 490		Phe Thr 495	Trp
aca cat aga agt Thr His Arg Ser 500	_				
act caa ctt cca Thr Gln Leu Pro 515		-	-		
att att gaa ggt Ile Ile Glu Gly 530					
gaa tct agt aat Glu Ser Ser Asn 545	_		-		-
gcc ttg tta caa Ala Leu Leu Gln		-	Arg Tyr Ala		
aac tta cga ctt Asn Leu Arg Leu 580	Phe Val Gln				
tac att aat aaa Tyr Ile Asn Lys 595	_		_		
ttt gat ctc gca Phe Asp Leu Ala 610		_			_
aat gaa ctt ata Asn Glu Leu Ile 625	23 2	-	-	_	
tat ata gat aag Tyr Ile Asp Lys			Gln Leu		1959
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<400> 48					
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- Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30
- Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45
- Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 60
- Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80
- Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95
- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350 \hspace{1.5cm}$

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp $370 \hspace{1cm} 375 \hspace{1cm} 380$

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405
410
415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435
440
445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile 625	Ile Gly Ala 0	Glu Ser Phe Val 635		ys Ile 640
Tyr Ile Asp Lys	Ile Glu Phe 1645	Ile Pro Val Gln 650	Leu	
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cca aat tca aca Pro Asn Ser Thr 35	Leu Glu Glu I			
act gaa gac agt Thr Glu Asp Ser 50				
gca gtt ggg aca Ala Val Gly Thr 65				
gga gtt cca ttt Gly Val Pro Phe			Tyr Gln Ser P	
aac act ata tgg Asn Thr Ile Trp 100				
caa gtt gaa gta Gln Val Glu Val 115	Leu Ile Asp I			
aaa gct ctt gca Lys Ala Leu Ala 130				

_		-			tcc Ser 150		-					-	_	-	•	480
		-			cga Arg			-					_	_	_	528
					atg Met											576
_					tat Tyr	-		-	-					-		624
		_	-		gtt Val			-	_						_	672
_	-	_	-		tat Tyr 230		-									720
	-		_	-	aat Asn				_						_	768
				-	gca Ala		-				-		-	-	-	816
-				_	tta Leu	_			_						_	864
-					aaa Lys		-			-			-	_		912
		_			ttt Phe 310						_					960
		_	_		gaa Glu				_						_	1008
		_			gaa Glu			_	_							1056
		_			aat Asn							_	_		_	1104
cct	agt	ata	gga	tct	agt	aag	aca	att	act	tcc	сса	ttt	tat	gga	gat	1152

H: 532973(BF8T01!.DOC) 134

Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp	
			-		_	caa Gln	_		•		_				-	1200
						aca Thr										1248
-				-	_	aaa Lys	_	_		_			_	_		1296
		_		_		caa Gln			-			_				1344
	-	-	-	-		tct Ser 455		_			_		-			1392
-	_			-		gca Ala		-		_					_	1440
_			-	_	-	cgt Arg	-									1488
		-	_	-	-	ttt Phe					_	_	-	_		1536
				-		aaa Lys	-		_	-				_		1584
						ttc Phe 535										1632
						gct Ala										1680
						cgt Arg										1728
						caa Gln										1776
						àat Asn										1824

gat Asp 610		_					,,,		_		-	-	1872
gaa Glu				_	_		_			-			1920
ata Ile	-	-	-			-		_	taa				1959

605

600

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595

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 50

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro 5

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 25

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 75

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 135

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn 150 155

Pro His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 · 285

Val Arg Leu Tyr Pro Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405
410
415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys	Phe	Leu	Met	Gln 485	Asp	Arg	Arg	Gly	Thr 490	Ile	Pro	Phe	Phe	Thr 495	Trp	
Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile	
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser	
Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys	
Glu 545	Ser	Ser	Asn	Ser	Ile 550	Ala	Lys	Phe	Lys	Val 555	Thr	Leu	Asn	Ser	Ala 560	
Ala	Leu	Leu	Gln	Arg 565	Tyr	Arg	Val	Arg	Ile 570	Arg	Tyr	Ala	Ser	Thr 575	Thr	
Asn	Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
Tyr	Ile	Asp	Lys	Ile 645	Glu	Phe	Ile	Pro	Val 650	Gln	Leu					
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Pro	Asn	Ser 35	Thr	Leu	Glu	Glu	Leu 40	Asn	Tyr	Lys	Glu	Phe 45	Leu	Arg	Met	
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											tat Tyr					28
											gct Ala					33
-	-	_	_		-	_					tat Tyr	-		-		38
_		_			_						ttc Phe 140	_	_		_	43:
						_					agt Ser	_	_	-		480
_	_		_								caa Gln	_	_	_		528
	_			_	_				_		aaa Lys		_		_	57
											cat His					62
											tat Tyr 220					67:
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_											aat Asn			_		768
			-	-		-				-	ttt Phe	~	_	-	_	816

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	cca gga tt Pro Gly Ph					_	1632	
	tca att go Ser Ile Al 55	a Lys Phe					1680	
	n cga tat co n Arg Tyr An 565		_	Tyr Ala			1728	
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gat ctc gca Asp Leu Ala 610				_		_	1872	
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu $85 \hspace{1cm} 90 \hspace{1cm} 95$

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln
100 105 110

Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys 115 120 125

Ala Leu Ala Glu Leu Gl
n Gly Leu Gl
n Asn Asn Phe Glu Asp Tyr Val $130 \\ 135 \\ 140$

Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser Lys 145 150 155 160

Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His 165 170 175

Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu 180 185 190

Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp 210 215 220

Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr 225 230 235 240

Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly 245 250 255

Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met 260 265 270

Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile 275 280 285

Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe 290 295 300

Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr 305 310 315 320

Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr 325 330 · 335 Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly 345 Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro 360 Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys 375 Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr 385 Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys 425 Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His 435 440 Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp 455 Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr 490 His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr 505 Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile 515 Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala 545 555 560 550 Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn 570 Leu Arg Leu Phe Val Gln Asn Ser Asn Asp Phe Leu Val Ile Tyr 585

Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr Phe

Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn

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630

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act gaa gac agt Thr Glu Asp Ser 50	-	Leu Asp Asn		_					
gca gtt ggg aca Ala Val Gly Thr 65									
gga gtt cca ttt Gly Val Pro Phe									
aac act ata tgg Asn Thr Ile Trp 100									
caa gtt gaa gta Gln Val Glu Val 115									
aaa gct ctt gca Lys Ala Leu Ala 130		Leu Gln Asn							
gtt aat gcg tta Val Asn Ala Leu									

145	150	155	160
	Arg Ile Arg Gl	a ctt ttt tct caa go u Leu Phe Ser Gln Al 170	
		t gca gtt tcc gga tt e Ala Val Ser Gly Ph 5	ne Glu Val
		et gca aat aca cat to a Ala Asn Thr His Lo 205	
		a gaa tgg gga tat to u Glu Trp Gly Tyr So 220	
-		a tta aaa ctt aca ca n Leu Lys Leu Thr Gi 235	
	l Asn Trp Tyr As	t gtt gga tta aat go n Val Gly Leu Asn G 250	
		a ttt aac cgt ttt co rs Phe Asn Arg Phe Ar 55 2	rg Arg Glu
-		t gta ctt ttc cca t e Val Leu Phe Pro Pl 285	
3 2		a aca gaa cta aca ac s Thr Glu Leu Thr A: 300	_
		at act ctt cag gag to on Thr Leu Gln Glu Ty 315	
	e Glu Asn Ser Il	et cga aaa cct cat to e Arg Lys Pro His Lo 330	
	=	eg cgt ctt caa cct ge ar Arg Leu Gln Pro G 5	
		et ggt aat tat gta ge er Gly Asn Tyr Val G 365	
	-	et act tcc cca ttt ta e Thr Ser Pro Phe Ty 380	

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	tat Tyr															1296
	aat Asn	_		_					-			_				1344
	gta Val 450	_	_	_	_			_			_		-			1392
_	gaa Glu			_		_		_		_					_	1440
	ttc Phe															1488
	cat His	_	-	_	-						-	_	-	_		1536
	caa Gln			_			_		_	_				-		1584
	att Ile 530															1632
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_	ttg Leu			_		-	_	-		_		-				1728
	tta Leu	-									_			_		1776
tac		224				t	222	ast	ant.	azit	++-	202	tat	caa	202	1824

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tat ata gat a Tyr Ile Asp L	-					1959
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Pro Asn Ser T 35	hr Leu Glu	Glu Leu Asn 40	Tyr Lys	Glu Phe L 45	eu Arg Me	et
Thr Glu Asp S 50	er Ser Thr	Glu Val Leu 55	Asp Asn	Ser Thr V	al Lys As	sp.
Ala Val Gly T 65	hr Gly Ile 70	Ser Val Val	Gly Gln 75	Ile Leu G	ly Val Va 80	
Gly Val Pro P	he Ala Gly 85	Ala Leu Thr	Ser Phe 90	Tyr Gln S	er Phe Le 95	eu
Asn Thr Ile T	rp Pro Ser 00	Asp Ala Asp 105	Pro Trp		he Met Al 10	.a
Gln Val Glu V 115	al Leu Ile	Asp Lys Lys 120	Ile Glu	Glu Tyr A 125	la Lys Se	er
Lys Ala Leu A 130	la Glu Leu	Gln Gly Leu 135	Gln Asn	Asn Phe G	lu Asp Ty	r'r
Val Asn Ala I 145	eu Asn Ser 150	Trp Lys Lys	Thr Pro 155	Leu Ser L	eu Arg Se 16	
Lys Arg Ser G	ln Asp Arg 165	Ile Arg Glu	Leu Phe 170	Ser Gln A	la Glu Se 175	er
His Phe Arg A	sn Ser Met	Pro Ser Phe	Ala Val	Ser Gly P	he Glu Va	al

180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 200 Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 215 Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 235 Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 250 Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 295 Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 330 Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 375 Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430 Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 455 Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp

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Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile	
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser	
Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys	
Glu 545	Ser	Ser	Asn	Ser	Ile 550	Ala	Lys	Phe	Lys	Val 555	Thr	Leu	Asn	Ser	Ala 560	
Ala	Leu	Leu	Gln	Arg 565	Tyr	Arg	Val	Arg	Ile 570	Arg	Tyr	Ala	Ser	Thr 575	Thr	
Asn	Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
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			aca Thr		-	_					-			-	_	144

35	40	45

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					gca Ala								624
	_	-		-	ttt Phe								672
					cat His 230								720
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					tgg Trp								816

										gat Asp		864
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							_			cca Pro		960
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										aga Arg		1104
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										caa Gln		1296
										ggc Gly		1344
										aca Thr		1392
										gaa Glu		1440
										tgg Trp 495		1488

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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Ala Gln 100 105 110

Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser Lys 115 120 125

Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr Val 130 135 140

Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Asn Pro 145 150 155 160

His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His 165 170 175

Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val Leu 180 185 190

Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu Asp 210 215 220

Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr 225 230 235 240

Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg Gly 245 250 255

Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met 260 265 270

Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile 275 280 285

Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe 290 295. 300

Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr 305 310 315 320

Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr 325 330 335

Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly 345 Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro 360 Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr 395 Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val 405 410 415 Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys 425 Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His 440 Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp 450 Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys 470 475 Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr 490 485 His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys Glu 535 530 Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala Ala 555 Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asp Phe Leu Val Ile Tyr 585 Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln Thr Phe 600 605 Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys Asn

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cca aa Pro As				_								_	144
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gga gt Gly Va			_		_								288
aac ac Asn Th													336
gtt ga Val Gl													384
gct ct Ala Le 13	u Āla												432
aat go Asn Al 145													480

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						tat Tyr										768
			_	-		gtc Val				-		_	_	_	_	816
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		_	_	_	-	cgt Arg										1488
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				_		aaa Lys	_	-	_							1824
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Asp	Leu 610	Ala	Thr	Thr	Asn	Ser 615	Asn	Met	Gly	Phe	Ser 620	Gly	Asp	Lys	Asn	
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Pro	Asn	Ser 35	Thr	Leu	Glu	Glu	Leu 40	Asn	Tyr	Lys	Glu	Phe 45	Leu	Arg	Met	
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Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr Thr 225 230 235 240

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Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu Met 260 265 270

Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp Ile 275 280 285

Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile Phe 290 295 300

Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro Thr 305 310 315 320

Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp Tyr 325 330 335

Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe Gly 340 345 350

Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg Pro 355 360 365

Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp Lys 370 375 380

Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val Tyr 385 390 395 400

Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys Val 405 410 415

Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln Lys
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Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly His
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440
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Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp 450 455 460

Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu Cys 465 470 475 480

Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp Thr 485 490 495

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					aat Asn									7	768
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gaa tct agt Glu Ser Ser 545		e Ála Lys		-		~	1680
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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met

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			Leu 580					585					590		
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Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

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Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

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		-			_	ttt Phe		-	_		_					1056
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Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

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Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

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Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650

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	-	_	_	tct Ser	_	-			_				_		_	192
				gga Gly												240
				gct Ala 85		_										288
				cca Pro	_	_	_	-			_	-		-	-	336
				ctg Leu												384
	_		-	gag Glu		_							_	_		432
		_		aat Asn			_					-	_		_	480
				ggt Gly 165												528
cat	ttt	cgt	aat	tcc	atg	ccg	tca	ttt	gca	gtt	tcc	aaa	ttc	gaa	gtg	576

His	Phe	Arg	Asn 180	Ser	Met	Pro	Ser	Phe 185	Ala	Val	Ser	Lys	Phe 190	Glu	Val	
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					gtt Val											672
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					aat Asn										_	768
				-	gca Ala		-				_		-	-	_	816
					tta Leu											864
					aaa Lys		_			-			_	-		912
					ttt Phe 310						_					960
		-	-		gaa Glu				_						_	1008
					gaa Glu											1056
					aat Asn											1104
					agt Ser											1152
					gta Val 390		_		_		_				-	1200
					aat Asn											1248

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		gat ttt agt caa tat Asp Phe Ser Gln Tyr 425	=
		tat gat tca aaa aga Tyr Asp Ser Lys Arg 445	Asn Asn Gly
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-	_	agt cat cag ctt aat Ser His Gln Leu Asr 475	2 2 2
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		aat aca att gat gct Asn Thr Ile Asp Ala 505	_
		tat gcc ttg tct tca Tyr Ala Leu Ser Ser 525	Gly Ala Ser
		gga gga aat tta cta Gly Gly Asn Leu Leu 540	
-	~	ttt aaa gtt aca tta Phe Lys Val Thr Leu 555	3
		aga ata cgc tat gct Arg Ile Arg Tyr Ala 570	
		tca aac aat gat ttt Ser Asn Asn Asp Phe 585	
		gat gat gat tta aca Asp Asp Asp Leu Thr 605	
		aat atg ggg ttc tcg Asn Met Gly Phe Ser 620	
		tet tte gtt tet aat Ser Phe Val Ser Asn 635	=

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Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp 225	Val	Ala	Glu	Phe	Tyr 230	His	Arg	Gln	Leu	Lys 235	Leu	Thr	Gln	Gln	Tyr 240
Thr	Asp	His	Cys	Val 245	Asn	Trp	Tyr	Asn	Val 250	Gly	Leu	Asn	Gly	Leu 255	Arg
Gly	Ser	Thr	Tyr 260	Asp	Ala	Trp	Val	Lys 265	Phe	Asn	Arg	Phe	Arg 270	Arg	Glu
Met	Thr	Leu 275	Thr	Val	Leu	Asp	Leu 280	Ile	Val	Leu	Phe	Pro 285	Phe	Tyr	Asp
Ile	Arg 290	Leu	Tyr	Ser	Lys	Gly 295	Val	Lys	Thr	Glu	Leu 300	Thr	Arg	Asp	Ile
Phe 305	Thr	Asp	Pro	Ile	Phe 310	Leu	Leu	Asn	Thr	Leu 315	Gln	Glu	Tyr	Gly	Pro 320
Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp
Tyr	Leu	Gln	Gly 340	Ile	Glu	Phe	His	Thr 345	Arg	Leu	Gln	Pro	Gly 350	Tyr	Phe
Gly	Lys	Asp 355	Ser	Phe	Asn	Tyr	Trp 360	Ser	Gly	Asn	Tyr	Val 365	Glu	Thr	Arg
Pro	Ser 370	Ile	Gly	Ser	Ser	Lys 375	Thr	Ile	Thr	Ser	Pro 380	Phe	Tyr	Gly	Asp
Lys 385	Ser	Thr	Glu	Pro	Val 390	Gln	Lys	Leu	Ser	Phe 395	Asp	Gly	Gln	Lys	Val 400
Tyr	Arg	Thr	Ile	Ala 405	Asn	Thr	Asp	Val	Ala 410	Ala	Trp	Pro	Asn	Gly 415	Lys
Val	Tyr	Leu	Gly 420	Val	Thr	Lys	Val	Asp 425	Phe	Ser	Gln	Tyr	Asp 430	Asp	Gln
Lys	Asn	Glu 435	Thr	Ser	Thr	Gln	Thr 440	Tyr	Asp	Ser	Lys	Arg 445	Asn	Asn	Gly
His	Val 450	Ser	Ala	Gln	Asp	Ser 455	Ile	Asp	Gln	Leu	Pro 460	Pro	Glu	Thr	Thr
Asp 465	Glu	Pro	Leu	Glu	Lys 470	Ala	Tyr	Ser	His	Gln 475	Leu	Asn	Tyr	Ala	Glu 480
Cys	Phe	Leu	Met	Gln 485	Asp	Arg	Arg	Gly	Thr 490	Ile	Pro	Phe	Phe	Thr 495	Trp
Thr	His	Arg	Ser 500	Val	Asp	Phe	Phe	Asn 505	Thr	Ile	Asp	Ala	Glu 510	Lys	Ile
Thr	Gln	Leu 515	Pro	Val	Val	Lys	Ala 520	Tyr	Ala	Leu	Ser	Ser 525	Gly	Ala	Ser

Ile	Ile 530	Glu	Gly	Pro	Gly	Phe 535	Thr	Gly	Gly	Asn	Leu 540	Leu	Phe	Leu	Lys	
Glu 545	Ser	Ser	Asn	Ser	Ile 550	Ala	Lys	Phe	Lys	Val 555	Thr	Leu	Asn	Ser	Ala 560	
Ala	Leu	Leu	Gln	Arg 565	Tyr	Arg	Val	Arg	Ile 570	Arg	Tyr	Ala	Ser	Thr 575	Thr	
Asn	Leu	Arg	Leu 580	Phe	Val	Gln	Asn	Ser 585	Asn	Asn	Asp	Phe	Leu 590	Val	Ile	
Tyr	Ile	Asn 595	Lys	Thr	Met	Asn	Lys 600	Asp	Asp	Asp	Leu	Thr 605	Tyr	Gln	Thr	
Phe	Asp 610	Leu	Ala	Thr	Thr	Asn 615	Ser	Asn	Met	Gly	Phe 620	Ser	Gly	Asp	Lys	
Asn 625	Glu	Leu	Ile	Ile	Gly 630	Ala	Glu	Ser	Phe	Val 635	Ser	Asn	Glu	Lys	Ile 640	
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	gtt Val															240

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					gat Asp	-			_	_	_	_	336
					gat Asp								384
					cag Gln 135								432
					tgg Trp								480
					ata Ile								528
	-			_	ccg Pro		_	_			_		576
-					gca Ala	-	_				_		624
Leu					ttt Phe 215								672
					cat His								720
		_	-		tgg Trp		-					-	768
					tgg Trp								816
atg Met					gat Asp		_					-	864
					ggg Gly 295								912

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	-				tca Ser					_					960
	_	-		_	aac Asn			_						-	1008
	_			_	ttt Phe		_	_		_					1056
	-				tat Tyr							_		_	1104
					aag Lys 375										1152
				-	caa Gln	_		_		-				-	1200
					aca Thr										1248
					aaa Lys				_			_	-		1296
	_				caa Gln			_			_				1344
-	_	-	_	_	tct Ser 455		-			_		_			1392
					gca Ala										1440
					cgt Arg										1488
					ttt Phe										1536
			-		aaa Lys	-		_	_				-		1584

att att gaa gg Ile Ile Glu Gl 530									1632
gaa tct agt aa Glu Ser Ser As 545		Ala Lys		-				-	1680
gcc ttg tta ca Ala Leu Leu Gl			Arg						1728
aac tta cga ct Asn Leu Arg Le 58	ı Phe Val				_		_		1776
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ttt gat ctc gc Phe Asp Leu Al 610									1872
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Pro Asn Ser Th	Leu Glu	Glu Leu 40	Asn T	Tyr Lys	Glu Ph 45		Arg	Met	
Thr Glu Asp Ser 50	Ser Thr	Glu Val 55	Leu A	Asp Asn	Ser Th	r Val	Lys	Asp	
Ala Val Gly The	Gly Ile 70	Ser Val	Val G	Gly Gln 75	Ile Le	u Gly	Val	Val 80	

Gly	Val	Pro	Phe	Ala	Gly	Ala	Leu	Thr	Ser	Phe	Tyr	Gln	Ser	Phe	Leu	
				85					90					95		

- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val
 180 185 '190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
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- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Arg Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

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cta tta aaa gat gct caa gtt ttt gga gaa gaa tgg gga tat tct tca Leu Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser 50 55 60	192
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tac act gac cat tgt gtt aat tgg tat aat gtt gga tta aat ggt tta Tyr Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu 85 90 95	288
aga ggt tca act tat gat gca tgg gtc aaa ttt aac cgt ttt cgc aga Arg Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg 100 105 110	336
gaa atg act tta act gta tta gat cta att gta ctt ttc cca ttt tat Glu Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr 115 120 125	384
gat att cgg tta tac tca aaa ggg gtt aaa aca gaa cta aca aga gac Asp Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp 130 135 140	432
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cca act ttt ttg agt ata gaa aac tct att cga aaa cct cat tta ttt Pro Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe 165 170 175	528
gat tat tta cag ggg att gaa ttt cat acg cgt ctt caa cct ggt tac Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr 180 185 190	576
ttt ggg aaa gat tct ttc aat tat tgg tct ggt aat tat gta gaa act Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr	624

		195					200					205				
					tct Ser	-	_									672
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					gct Ala											768
_	-				gtt Val	_		_	-		_			-	_	816
					agt Ser											864
		-	-	-	cag Gln	-			_			_		-		912
	_	_			gaa Glu 310		-				_					960
					cag Gln											1008
			-	_	gta Val	-						_	_	_	_	1056
			_		gta Val					-	_				-	1104
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189

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Val Le	eu Phe 35	Leu	Pro	Thr	Tyr	Ala 40	Gln	Ala	Ala	Asn	Thr 45	His	Leu	Leu		
Leu Le 50	eu Lys)	Asp	Ala	Gln	Val 55	Phe	Gly	Glu	Glu	Trp 60	Gly	Tyr	Ser	Ser		
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Tyr Th	nr Asp	His	Cys 85	Val	Asn	Trp	Tyr	Asn 90	Val	Gly	Leu	Asn	Gly 95	Leu		
Arg Gl	ly Ser	Thr 100	Tyr	Asp	Ala	Trp	Val 105	Lys	Phe	Asn	Arg	Phe 110	Arg	Arg		
Glu Me	et Thr 115	Leu	Thr	Val	Leu	Asp 120	Leu	Ile	Val	Leu	Phe 125	Pro	Phe	Tyr		
Asp II		Leu	Tyr	Ser	Lys 135	Gly	Val	Lys	Thr	Glu 140	Leu	Thr	Arg	Asp		
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Pro	Thr	Phe	ьeu	Ser	тте	GIU	Asn	Ser	тте	Arg	ьуs	Pro	Hls	Leu	Phe	
				165					170					175		

- Asp Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr 180 185 190
- Phe Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr 195 200 205
- Arg Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly 210 215 220
- Asp Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys 225 230 235 240
- Val Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly 245 250 255
- Lys Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp 260 265 270
- Gln Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn 275 280 285
- Gly His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr 290 295 300
- Thr Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala 305 310 315 320
- Glu Cys Phe Leu Met Gln Asp Arg Gly Thr Ile Pro Phe Phe Thr 325 330 335
- Trp Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys 340 345 350
- Ile Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala 355 360 365
- Ser Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu $370 \hspace{1cm} 375 \hspace{1cm} 380$
- Lys Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser 385 390 395 400
- Ala Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr 405 410 415
- Thr Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val
 420 425 430
- Ile Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Asp Leu Thr Tyr Gln
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- Thr Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp 450 455 460

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<222> (17)..(17)
\langle 223 \rangle N = A, T, C (16% each); G (52%)
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<223> N = A, T, G, C (25% each)
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<222> (33)..(33)
\langle 223 \rangle N = A, G, C (6% each); T (82%)
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<222>
      (34)..(34)
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      (35)..(35)
<223> N = A, G, C (6% each); T (82%)
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      (36)..(36)
<223>
       N = A, T, G (6% each); C (82%)
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      (37)..(37)
<223> N = A, G, C (6% each); T (82%)
<220>
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<222>
      (38)..(38)
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\langle 223 \rangle N = A, T, G (6% each); C (82%)
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\langle 223 \rangle N = A, T, C (6% each); G (82%)
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<223> N = A, T, G, C (25% each)
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      (43)..(43)
\langle 223 \rangle N = A, T, G (6% each); C (82%)
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<222> (44)..(44)
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                                                                         60
                                                                         64
gaat
<210> 77
<211> 40
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<213> Artificial sequence
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<400> 77
                                                                         40
ggtcacctag gtctctcttc caggaattta acgcattaac
<210> 78
<211>
      65
<212> DNA
<213> Artificial sequence
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<222>
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<223> N = T, G, C (6% each); A (82%)
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<220>
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      (25)..(25)
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<220>
<221> misc feature
<222> (26)..(26)
<223> N = T, G, C (6% each); A (82%)
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       (27)..(27)
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<223> N = A, G, C (6% each); T (82%)
<220>
<221> misc feature
      (30)..(30)
<222>
<223> N = A, G, C (6% each); T (82%)
<220>
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<222> (31)..(31)
<223> N = T, G, C (6% each); A (82%)
<220>
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      misc_feature
<222>
       (32)..(33)
```

```
<223> N = A, T, C (6% each); G (82%)
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      (34)..(34)
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<222> (37)..(37)
<223> N = A, G, C (6% each); T (82%)
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<221> misc_feature
<222>
      (38)..(38)
<223> N = T, G, C (6% each); A (82%)
<220>
<221> misc_feature
<222> (39)..(39)
\langle 223 \rangle N = A, T, G (1% each); C (97%)
<220>
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<222>
      (40)..(40)
<223> N = T, G, C (6% each); A (82%)
<220>
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<222> (41)..(41)
<223> N = A, T, C (6% each); G (82%)
<220>
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<222> (42)..(42)
\langle 223 \rangle N = A, G, C (6% each); T (82%)
<220>
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<223> N = T, G, C (6% each); A (82%)
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<222> (45)..(45)
<223> N = A, T, G, C (25% each)
<220>
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      (46)..(48)
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```

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                                                                      60
ctaac
                                                                      65
<210> 79
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       36
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                                                                      36
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\langle 223 \rangle N = A, T, G (6% each); C (82%)
<220>
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<223> N = A, G, C (6% each); T (82%)
<220>
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<223> N = A, T, G (6% each); C (82%)
<220>
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<222> (29)..(30)
<223> N = T, G, C (6% each); A (82%)
<220>
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<222> (31)..(31)
<223> N = A, G, C (6% each); T (82%)
```

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<222> (32)..(32)
<223> N = T, G, C (6% each); A (82%)
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<220>
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<223> N = A, T, G (6% each); C (82%)
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\langle 223 \rangle N = A, T, G (6% each); C (82%)
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<223> N = A, T, G (6% each); C (82%)
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\langle 223 \rangle N = A, T, G (6% each); C (82%)
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      (39)..(39)
<223> N = T, G, C (6% each); A (82%)
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<222> (40)..(40)
<223> N = A, T, C (6% each); G (82%)
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\langle 223 \rangle N = A, C (8% each); T (1%); G (83%)
<220>
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       (42)..(42)
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```
<222> (43)..(43)
<223> N = A, T, C (6% each); G (82%)
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<223> N = A, G, C (6% each); T (82%)
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\langle 223 \rangle N = T, G, C (6% each); A (82%)
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                                                                       60
                                                                       63
gag
<210> 81
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<223> N = A, G, C (6% each); T (82%)
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<222> (29)..(29)
<223> N = T, G, C (6% each); A (82%)
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<222> (30)..(30)
<223> N = A, T, G (1% each); C (97%)
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      (34)..(35)
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<223> N = T, G, C (6% each); A (82%)
<220>
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<222> (42)..(42)
<223> N = A, G, C (6% each); T (82%)
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gaatttcata cgcgtcttca acctggtnnn nnnnnnnnn nntctttcaa ttattggtct
                                                                      60
                                                                       62
gg
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      73
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<223> N = A, T, G (6% each); C (82%)
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      (46)..(46)
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      (47)..(48)
\langle 223 \rangle N = T, G, C (6% each); A (82%)
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\langle 223 \rangle N = A, G, C (6% each); T (82%)
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                                                                          60
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                                                                          73
tttaggtgtt acg
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<400> 83
                                                                          20
ggagttccat ttgctggggc
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25
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ccgctacgtc tgtatta
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ataatggaag cacctga
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       (35)..(35)
\langle 223 \rangle N = A, T, C (6% each); G (82%)
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       (36)..(36)
\langle 223 \rangle N = A, G, C (6% each); T (82%)
<220>
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\langle 223 \rangle N = A, T, C (6% each); G (82%)
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                                                                       60
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      40
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                                                                       40
atccagttgg gtctctaaga aacaaaccgc gtaattaagc
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      94
<211> 20
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                                                                       20
cctcaagggt tataacatcc
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\langle 223 \rangle N = A, G (8% each); T (2%); C (82%)
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<223> N = A (82%); T (2%); G,C (8% each)
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\langle 223 \rangle N = T, G, C (6% each); A (82%)
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                                                                     55
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<212> PRT
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<400> 96
Ser Lys Arg Ser Gln Asp Arg
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Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro
                                                                       96
aac agt gaa ttg caa act aac cat aat caa tat cct tta gct gac aat
Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn
            20
                                                                      144
cca aat tca aca cta qaa qaa tta aat tat aaa gaa ttt tta aga atg
Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met
        35
                                                                      192
act qaa qac aqt tct acq qaa qtq cta qac aac tct aca gta aaa gat
Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp
    50
                        55
qca gtt ggg aca gga att tct gtt gta ggg cag att tta ggt gtt gta
                                                                      240
Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val
                    70
                                                                      288
gga gtt cca ttt gct ggg gca ctc act tca ttt tat caa tca ttt ctt
Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu
                                    90
```

					-	gat Asp	-	-			_	_				336
	-	_	-	_		gat Asp	_									384
	-		_			cag Gln 135							-	-		432
-						tgg Trp	_					-	_	-	_	480
	-	_		_	_	ata Ile		-					_	_		528
		_			_	ccg Pro			_	_				_	-	576
_						gca Ala		-	-					_		624
						ttt Phe 215		-								672
-	_	_	-			cat His	-									720
	-		-	_		tgg Trp			-						_	768
				_	_	tgg Trp	-				_		-	_	_	816
						gat Asp										864
						ggg Gly 295	_			-			_	-		912
	_	_				tca Ser					_					960
act	ttt	ttg	agt	ata	gaa	aac	tct	att	cga	aaa	cct	cat	tta	ttt	gat	1008

Thr	Phe	Leu	Ser	Ile 325	Glu	Asn	Ser	Ile	Arg 330	Lys	Pro	His	Leu	Phe 335	Asp	
											caa Gln					1056
		-									tat Tyr	_	_		_	1104
	_				_	_					cca Pro 380				_	1152
			_		-		_		_		gat Asp				_	1200
				_			_	_	, ,	_	tgg Trp	_			_	1248
_				_	_		-	_		-	caa Gln		_			1290
		_		_					-		aaa Lys	-				134
	-	_	-	_							ccg Pro 460		-			1392
_	_			_		_		-		_	ctt Leu				_	1440
_			_	_	-	-	-				cca Pro					1488
											gat Asp					1530
											tct Ser					1584
		-									tta Leu 540					1632
-		_				-				_	aca Thr				_	1680

545	550		555	560
			cgc tat gct tct Arg Tyr Ala Ser	
			aat gat ttt ctt Asn Asp Phe Leu 590	
			gat tta aca tat Asp Leu Thr Tyr 605	
		n Ser Asn Met	ggg ttc tcg ggt Gly Phe Ser Gly 620	_
-		-	gtt tct aat gaa Val Ser Asn Glu 635	
tat ata gat aag Tyr Ile Asp Lys	•	_		1959
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	thuringien	sis		
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Asp Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val 65 70 75 80

Val Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe 85 90 95

Leu Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met 100 105 110

Ala Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys 115 120 125

Ser Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp 130 135 140

Tyr Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg 145 150 155 160

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Ser His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu 180 185 190

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ttttatqqaq ataaatctac tqaacctqta caaaaqctaa qctttqatqq acaaaaaqtt 1200 tatcqaacta tagctaatac agacgtagcg gcttggccga atggtaaggt atatttaggt 1260 qttacqaaaq ttqattttaq tcaatatqat qatcaaaaaa atqaaactag tacacaaaca 1320 tatqattcaa aaagaaacaa tqqccatqta aqtqcacaqq attctattqa ccaattaccq 1380 ccaqaaacaa caqatqaacc acttgaaaaa gcatatagtc atcagcttaa ttacqcqqaa 1440 tgtttcttaa tgcaggaccg tcgtggaaca attccatttt ttacttggac acatagaagt 1500 gtagactttt ttaatacaat tgatgctgaa aagattactc aacttccagt agtgaaagca 1560 tatgccttgt cttcaggtgc ttccattatt gaaggtccag gattcacagg aggaaattta 1620 ctattcctaa aagaatctag taattcaatt gctaaattta aagttacatt aaattcagca 1680 gccttgttac aacgatatcg tgtaagaata cgctatgctt ctaccactaa cttacgactt 1740 tttgtgcaaa attcaaacaa tgattttctt gtcatctaca ttaataaaac tatgaataaa 1800 qatqatqatt taacatatca aacatttqat ctcqcaacta ctaattctaa tatqqqqttc 1860 tcgggtgata agaatgaact tataatagga gcagaatctt tcgtttctaa tgaaaaaatc 1920 tatatagata agatagaatt tatcccagta caattgtaa 1959

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<210> 108
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<220>

<223> Recombinant delta endotoxin

<400> 108

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro $1 \ \ \, 5 \ \ \, 10 \ \ \, 15$

Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

<211> 652

<212> PRT

<213> Artificial sequence

Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr Arg Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg \$245\$ \$250\$ \$255\$

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 260 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285

Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

Phe Thr Asp Pro Ile Phe Leu Leu Thr Thr Leu Gln Lys Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

- Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys 405 410 415
- Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln 420 425 430
- Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445
- His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460
- Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480
- Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
 485 490 495
- Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510
- Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525
- Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540
- Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560
- Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575
- Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590
- Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605
- Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620
- Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640
- Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650
- <210> 109
- <211> 649
- <212> PRT
- <213> Artificial sequence
- <220>
- <223> Recombinant delta endotoxin

- Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Ala Thr Glu

 1 5 10 15
- Asn Asn Glu Val Ser Asn Asn His Ala Gln Tyr Pro Leu Ala Asp Thr 20 25 30
- Pro Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Arg Thr Thr 35 40 45
- Asp Asn Asn Val Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp Ala Ile 50 55 60
- Gln Lys Gly Ile Ser Ile Ile Gly Asp Leu Leu Gly Val Val Gly Phe 70 75 80
- Pro Tyr Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Leu Leu Asn Thr 85 90 95
- Ile Trp Pro Gly Glu Asp Pro Leu Lys Ala Phe Met Gln Gln Val Glu
 100 105 110
- Ala Leu Ile Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asp Lys Ala Thr 115 120 125
- Ala Glu Leu Gln Gly Leu Lys Asn Val Phe Lys Asp Tyr Val Ser Ala 130 135 140
- Leu Asp Ser Trp Asp Lys Thr Pro Leu Thr Leu Arg Asp Gly Arg Ser 145 150 155 160
- Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg 165 170 175
- Arg Ser Met Pro Ser Phe Ala Val Ser Gly Tyr Glu Val Leu Phe Leu 180 185 190
- Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu Lys Asp 195 200 205
- Ala Gln Ile Tyr Gly Thr Asp Trp Gly Tyr Ser Thr Asp Asp Leu Asn 210 215 220
- Glu Phe His Thr Lys Gln Lys Asp Leu Thr Ile Glu Tyr Thr Asn His 225 230 235 240
- Cys Ala Lys Trp Tyr Lys Ala Gly Leu Asp Lys Leu Arg Gly Ser Thr 245 250 255
- Tyr Glu Glu Trp Val Lys Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu 260 265 270
- Thr Val Leu Asp Leu Ile Thr Leu Phe Pro Leu Tyr Asp Val Arg Thr 275 280 285
- Tyr Thr Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Val Leu Thr Asp

290 295 300

Pro Ile Val Ala Val Asn Asn Met Asn Gly Tyr Gly Thr Thr Phe Ser 315 310 Asn Ile Glu Asn Tyr Ile Arg Lys Pro His Leu Phe Asp Tyr Leu His Ala Ile Gln Phe His Ser Arg Leu Gln Pro Gly Tyr Phe Gly Thr Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Ser Thr Arg Ser Ser Ile 360 365 Gly Ser Asp Glu Ile Ile Arg Ser Pro Phe Tyr Gly Asn Lys Ser Thr 375 Leu Asp Val Gln Asn Leu Glu Phe Asn Gly Glu Lys Val Phe Arg Ala 395 Val Ala Asn Gly Asn Leu Ala Val Trp Pro Val Gly Thr Gly Gly Thr 410 Lys Ile His Ser Gly Val Thr Lys Val Gln Phe Ser Gln Tyr Asn Asp 420 Arg Lys Asp Glu Val Arg Thr Gln Thr Tyr Asp Ser Lys Arg Asn Val 440 Gly Gly Ile Val Phe Asp Ser Ile Asp Gln Leu Pro Pro Ile Thr Thr 455 Asp Glu Ser Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Val Arg 475 Cys Phe Leu Leu Gln Gly Gly Arg Gly Ile Ile Pro Val Phe Thr Trp 490 485 Thr His Lys Ser Val Asp Phe Tyr Asn Thr Leu Asp Ser Glu Lys Ile Thr Gln Ile Pro Phe Val Lys Ala Phe Ile Leu Val Asn Ser Thr Ser 520 Val Val Ala Gly Pro Gly Phe Thr Gly Gly Asp Ile Ile Lys Cys Thr 530 535 540 Asn Gly Ser Gly Leu Thr Leu Tyr Val Thr Pro Ala Pro Asp Leu Thr 545 550 Tyr Ser Lys Thr Tyr Lys Ile Arg Ile Arg Tyr Ala Ser Thr Ser Gln 570 Val Arg Phe Gly Ile Asp Leu Gly Ser Tyr Thr His Ser Ile Ser Tyr 580 585 590

Phe Asp Lys Thr Met Asp Lys Gly Asn Thr Leu Thr Tyr Asn Ser Phe

595 600 605

Asn Leu Ser Ser Val Ser Arg Pro Ile Glu Ile Ser Gly Gly Asn Lys 610 620

Ile Gly Val Ser Val Gly Gly Ile Gly Ser Gly Asp Glu Val Tyr Ile 625 630 635 640

Asp Lys Ile Glu Phe Ile Pro Met Asp 645

<210> 110

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 110

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

As Ser Glu Leu Pro Thr As His As Gln Tyr Pro Leu Ala Asp As 20 25 30

Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45

Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60

Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80

Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

Asp Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110

Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125

Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140

Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160

Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175

His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190

Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205

Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220

Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240

Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255

Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Arg Glu 265 270

Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285

Val Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300

Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320

Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335

Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Ser 340 345 350

Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365

Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380

Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405 410 415

Ile Tyr Phe Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly 435 440 445

His Val Gly Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp
485 490 495

- Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile
 500
 505
 510
- Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525
- Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540
- Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560
- Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575
- Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Ile Val Ile 580 585 590
- Tyr Ile Asn Lys Thr Met Asn Ile Asp Asp Asp Leu Thr Tyr Gln Thr 595 600 605
- Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Thr 610 615 620
- Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640
- Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650
- <210> 111
- <211> 652
- <212> PRT
- <213> Artificial sequence
- <220>
- <223> Recombinant delta endotoxin
- <400> 111
- Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Val Thr Pro 1 5 10 15
- Asn Ser Glu Leu Gln Thr Asn His Asn Gln Tyr Pro Leu Ala Asp Asn 20 25 30
- Pro Asn Ser Thr Leu Glu Glu Leu Asn Tyr Lys Glu Phe Leu Arg Met 35 40 45
- Thr Glu Asp Ser Ser Thr Glu Val Leu Asp Asn Ser Thr Val Lys Asp 50 55 60
- Ala Val Gly Thr Gly Ile Ser Val Val Gly Gln Ile Leu Gly Val Val 65 70 75 80
- Gly Val Pro Phe Ala Gly Ala Leu Thr Ser Phe Tyr Gln Ser Phe Leu 85 90 95

- Asn Thr Ile Trp Pro Ser Asp Ala Asp Pro Trp Lys Ala Phe Met Ala 100 105 110
- Gln Val Glu Val Leu Ile Asp Lys Lys Ile Glu Glu Tyr Ala Lys Ser 115 120 125
- Lys Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Phe Glu Asp Tyr 130 135 140
- Val Asn Ala Leu Asn Ser Trp Lys Lys Thr Pro Leu Ser Leu Arg Ser 145 150 155 160
- Lys Arg Ser Gln Asp Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser 165 170 175
- His Phe Arg Asn Ser Met Pro Ser Phe Ala Val Ser Lys Phe Glu Val 180 185 190
- Leu Phe Leu Pro Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Leu Leu 195 200 205
- Leu Lys Asp Ala Gln Val Phe Gly Glu Glu Trp Gly Tyr Ser Ser Glu 210 215 220
- Asp Val Ala Glu Phe Tyr His Arg Gln Leu Lys Leu Thr Gln Gln Tyr 225 230 235 240
- Thr Asp His Cys Val Asn Trp Tyr Asn Val Gly Leu Asn Gly Leu Arg 245 250 255
- Gly Ser Thr Tyr Asp Ala Trp Val Lys Phe Asn Arg Phe Arg Glu 260 265 270
- Met Thr Leu Thr Val Leu Asp Leu Ile Val Leu Phe Pro Phe Tyr Asp 275 280 285
- Ile Arg Leu Tyr Ser Lys Gly Val Lys Thr Glu Leu Thr Arg Asp Ile 290 295 300
- Phe Thr Asp Pro Ile Phe Ser Leu Asn Thr Leu Gln Glu Tyr Gly Pro 305 310 315 320
- Thr Phe Leu Ser Ile Glu Asn Ser Ile Arg Lys Pro His Leu Phe Asp 325 330 335
- Tyr Leu Gln Gly Ile Glu Phe His Thr Arg Leu Gln Pro Gly Tyr Phe 340 345 350
- Gly Lys Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Glu Thr Arg 355 360 365
- Pro Ser Ile Gly Ser Ser Lys Thr Ile Thr Ser Pro Phe Tyr Gly Asp 370 375 380
- Lys Ser Thr Glu Pro Val Gln Lys Leu Ser Phe Asp Gly Gln Lys Val 385 390 395 400

Tyr Arg Thr Ile Ala Asn Thr Asp Val Ala Ala Trp Pro Asn Gly Lys
405
410
415

Val Tyr Leu Gly Val Thr Lys Val Asp Phe Ser Gln Tyr Asp Asp Gln
420 425 430

Lys Asn Glu Thr Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Asn Gly
435 440 445

His Val Ser Ala Gln Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr 450 455 460

Asp Glu Pro Leu Glu Lys Ala Tyr Ser His Gln Leu Asn Tyr Ala Glu 465 470 475 480

Cys Phe Leu Met Gln Asp Arg Arg Gly Thr Ile Pro Phe Phe Thr Trp 485 490 495

Thr His Arg Ser Val Asp Phe Phe Asn Thr Ile Asp Ala Glu Lys Ile 500 505 510

Thr Gln Leu Pro Val Val Lys Ala Tyr Ala Leu Ser Ser Gly Ala Ser 515 520 525

Ile Ile Glu Gly Pro Gly Phe Thr Gly Gly Asn Leu Leu Phe Leu Lys 530 535 540

Glu Ser Ser Asn Ser Ile Ala Lys Phe Lys Val Thr Leu Asn Ser Ala 545 550 555 560

Ala Leu Leu Gln Arg Tyr Arg Val Arg Ile Arg Tyr Ala Ser Thr Thr 565 570 575

Asn Leu Arg Leu Phe Val Gln Asn Ser Asn Asn Asp Phe Leu Val Ile 580 585 590

Tyr Ile Asn Lys Thr Met Asn Lys Asp Asp Leu Thr Tyr Gln Thr 595 600 605

Phe Asp Leu Ala Thr Thr Asn Ser Asn Met Gly Phe Ser Gly Asp Lys 610 615 620

Asn Glu Leu Ile Ile Gly Ala Glu Ser Phe Val Ser Asn Glu Lys Ile 625 630 635 640

Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Gln Leu 645 650

<210> 112

<211> 659

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

- Met Ile Arg Met Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu 1 5 10 15
- Tyr Asp Thr Ile Lys Val Thr Pro Asn Ser Glu Leu Pro Thr Asn His 20 25 30
- Asn Gln Tyr Pro Leu Ala Asp Asn Pro Asn Ser Thr Leu Glu Glu Leu 35 40 45
- Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Ser Thr Glu Val 50 55 60
- Leu Asp Ser Ser Thr Val Lys Asp Ala Val Gly Thr Gly Ile Ser Val 65 70 75 80
- Val Gly Gln Ile Leu Gly Val Val Gly Val Pro Phe Ala Gly Ala Leu 85 90 95
- Thr Ser Phe Tyr Gln Ser Phe Leu Asn Ala Ile Trp Pro Ser Asp Ala 100 105 110
- Asp Pro Trp Lys Ala Phe Met Ala Gln Val Glu Val Leu Ile Asp Lys 115 120 125
- Lys Ile Glu Glu Tyr Ala Lys Ser Lys Ala Leu Ala Glu Leu Gln Gly 130 135 140
- Leu Gln Asn Asn Phe Glu Asp Tyr Val Asn Ala Leu Asp Ser Trp Lys 145 150 155 160
- Lys Ala Pro Val Asn Leu Arg Ser Arg Arg Ser Gln Asp Arg Ile Arg 165 170 175
- Glu Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser 180 185 190
- Phe Ala Val Ser Lys Phe Glu Val Leu Phe Leu Pro Thr Tyr Ala Gln 195 200 205
- Ala Ala Asn Thr His Leu Leu Leu Leu Lys Asp Ala Gln Val Phe Gly 210 215 220
- Glu Glu Trp Gly Tyr Ser Ser Glu Asp Ile Ala Glu Phe Tyr Gln Arg 225 230 235 240
- Gln Leu Lys Leu Thr Gln Gln Tyr Thr Asp His Cys Val Asn Trp Tyr 245 250 255
- Asn Val Gly Leu Asn Ser Leu Arg Gly Ser Thr Tyr Asp Ala Trp Val 260 265 270
- Lys Phe Asn Arg Phe Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu 275 280 285

- Ile Val Leu Phe Pro Phe Tyr Asp Val Arg Leu Tyr Ser Lys Gly Val 290 295 300
- Lys Thr Glu Leu Thr Arg Asp Ile Phe Thr Asp Pro Ile Phe Thr Leu 305 310 315 320
- Asn Ala Leu Gln Glu Tyr Gly Pro Thr Phe Ser Ser Ile Glu Asn Ser 325 330 335
- Ile Arg Lys Pro His Leu Phe Asp Tyr Leu Arg Gly Ile Glu Phe His 340 345 350
- Thr Arg Leu Arg Pro Gly Tyr Ser Gly Lys Asp Ser Phe Asn Tyr Trp 355 360 365
- Ser Gly Asn Tyr Val Glu Thr Arg Pro Ser Ile Gly Ser Asn Asp Thr 370 375 380
- Ile Thr Ser Pro Phe Tyr Gly Asp Lys Ser Ile Glu Pro Ile Gln Lys 385 390 395 400
- Leu Ser Phe Asp Gly Gln Lys Val Tyr Arg Thr Ile Ala Asn Thr Asp 405 410 415
- Ile Ala Ala Phe Pro Asp Gly Lys Ile Tyr Phe Gly Val Thr Lys Val 420 425 430
- Asp Phe Ser Gln Tyr Asp Asp Gln Lys Asn Glu Thr Ser Thr Gln Thr 435 440 445
- Tyr Asp Ser Lys Arg Tyr Asn Gly Tyr Leu Gly Ala Gln Asp Ser Ile 450 460
- Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Ala Tyr 465 470 475 480
- Ser His Gln Leu Asn Tyr Ala Glu Cys Phe Leu Met Gln Asp Arg Arg 485 490 495
- Gly Thr Ile Pro Phe Phe Thr Trp Thr His Arg Ser Val Asp Phe Phe 500 505 510
- Asn Thr Ile Asp Ala Glu Lys Ile Thr Gln Leu Pro Val Val Lys Ala 515 520 525
- Tyr Ala Leu Ser Ser Gly Ala Ser Ile Ile Glu Gly Pro Gly Phe Thr 530 535 540
- Gly Gly Asn Leu Leu Phe Leu Lys Glu Ser Ser Asn Ser Ile Ala Lys 545 550 555 560
- Phe Lys Val Thr Leu Asn Ser Ala Ala Leu Leu Gln Arg Tyr Arg Val
 565 570 575
- Arg Ile Arg Tyr Ala Ser Thr Thr Asn Leu Arg Leu Phe Val Gln Asn 580 585 590

Ser Asn Asp Phe Leu Val Ile Tyr Ile Asn Lys Thr Met Asn Ile 595 600

Asp Gly Asp Leu Thr Tyr Gln Thr Phe Asp Phe Ala Thr Ser Asn Ser 610 620

Asn Met Gly Phe Ser Gly Asp Thr Asn Asp Phe Ile Ile Gly Ala Glu 625 630 635 640

Ser Phe Val Ser Asn Glu Lys Ile Tyr Ile Asp Lys Ile Glu Phe Ile 645 650 655

Pro Val Gln

<210> 113

<211> 652

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant delta endotoxin

<400> 113

Met Ile Arg Lys Gly Gly Arg Lys Met Asn Pro Asn Asn Arg Ser Glu

5 10 15

His Asp Thr Ile Lys Thr Thr Glu Asn Asn Glu Val Pro Thr Asn His 20 25 30

Val Gln Tyr Pro Leu Ala Glu Thr Pro Asn Pro Thr Leu Glu Asp Leu 35 40 45

Asn Tyr Lys Glu Phe Leu Arg Met Thr Ala Asp Asn Asn Thr Glu Ala 50 60

Leu Asp Ser Ser Thr Thr Lys Asp Val Ile Gln Lys Gly Ile Ser Val 65 70 75 80

Val Gly Asp Leu Leu Gly Val Val Gly Phe Pro Phe Gly Gly Ala Leu 85 90 95

Val Ser Phe Tyr Thr Asn Phe Leu Asn Thr Ile Trp Pro Ser Glu Asp 100 105 110

Pro Trp Lys Ala Phe Met Glu Gln Val Glu Ala Leu Met Asp Gln Lys 115 120 125

Ile Ala Asp Tyr Ala Lys Asn Lys Ala Leu Ala Glu Leu Gln Gly Leu 130 135 140

Gln Asn Asn Val Glu Asp Tyr Val Ser Ala Leu Ser Ser Trp Gln Lys 145 150 155 160

Asn Pro Val Ser Ser Arg Asn Pro His Ser Gln Gly Arg Ile Arg Glu 165 170 175

Leu Phe Ser Gln Ala Glu Ser His Phe Arg Asn Ser Met Pro Ser Phe 180 185 190

- Ala Ile Ser Gly Tyr Glu Val Leu Phe Leu Thr Thr Tyr Ala Gln Ala 195 200 205
- Ala Asn Thr His Leu Phe Leu Leu Lys Asp Ala Gln Ile Tyr Gly Glu 210 215 220
- Glu Trp Gly Tyr Glu Lys Glu Asp Ile Ala Glu Phe Tyr Lys Arg Gln 225 230 235 240
- Leu Lys Leu Thr Gln Glu Tyr Thr Asp His Cys Val Lys Trp Tyr Asn 245 250 255
- Val Gly Leu Asp Lys Leu Arg Gly Ser Ser Tyr Glu Ser Trp Val Asn 260 265 270
- Phe Asn Arg Tyr Arg Arg Glu Met Thr Leu Thr Val Leu Asp Leu Ile 275 280 285
- Ala Leu Phe Pro Leu Tyr Asp Val Arg Leu Tyr Pro Lys Glu Val Lys 290 295 300
- Thr Glu Leu Thr Arg Asp Val Leu Thr Asp Pro Ile Val Gly Val Asn 305 310 315 320
- Asn Leu Arg Gly Tyr Gly Thr Thr Phe Ser Asn Ile Glu Asn Tyr Ile 325 330 335
- Arg Lys Pro His Leu Phe Asp Tyr Leu His Arg Ile Gln Phe His Thr 340 345 350
- Arg Phe Gln Pro Gly Tyr Tyr Gly Asn Asp Ser Phe Asn Tyr Trp Ser 355 360 365
- Gly Asn Tyr Val Ser Thr Arg Pro Ser Ile Gly Ser Asn Asp Ile Ile 370 375 380
- Thr Ser Pro Phe Tyr Gly Asn Lys Ser Ser Glu Pro Val Gln Asn Leu 385 390 395 400
- Glu Phe Asn Gly Glu Lys Val Tyr Arg Ala Val Ala Asn Thr Asn Leu 405 410 415
- Ala Val Trp Pro Ser Ala Val Tyr Ser Gly Val Thr Lys Val Glu Phe
 420 425 430
- Ser Gln Tyr Asn Asp Gln Thr Asp Glu Ala Ser Thr Gln Thr Tyr Asp 435 440 445
- Ser Lys Arg Asn Val Gly Ala Val Ser Trp Asp Ser Ile Asp Gln Leu 450 455 460
- Pro Pro Glu Thr Thr Asp Glu Pro Leu Glu Lys Gly Tyr Ser His Gln 465 470 475 480
- Leu Asn Tyr Val Met Cys Phe Leu Met Gln Gly Ser Arg Gly Thr Ile 485 490 495

- Pro Val Leu Thr Trp Thr His Lys Ser Val Asp Phe Phe Asn Met Ile 500 505 510
- Asp Ser Lys Lys Ile Thr Gln Leu Pro Leu Val Lys Ala Tyr Lys Leu 515 520 525
- Gln Ser Gly Ala Ser Val Val Ala Gly Pro Arg Phe Thr Gly Gly Asp 530 535 540
- Ile Ile Gln Cys Thr Glu Asn Gly Ser Ala Ala Thr Ile Tyr Val Thr 545 550 555 560
- Pro Asp Val Ser Tyr Ser Gln Lys Tyr Arg Ala Arg Ile His Tyr Ala 565 570 575
- Ser Thr Ser Gln Ile Thr Phe Thr Leu Ser Leu Asp Gly Ala Pro Phe 580 585 590
- Asn Gln Tyr Tyr Phe Asp Lys Thr Ile Asn Lys Gly Asp Thr Leu Thr 595 600 605
- Tyr Asn Ser Phe Asn Leu Ala Ser Phe Ser Thr Pro Phe Glu Leu Ser 610 620
- Gly Asn Asn Leu Gln Ile Gly Val Thr Gly Leu Ser Ala Gly Asp Lys 625 630 635 640